

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2004, 14:21:01 ; Search time 22 Seconds
(without alignment)
434.648 Million cell updates/sec

Title: US-09-965-529-26
Perfect score: 1200
Sequence: 1 MKWVAPTRFYSNCCLCCH.....YDDATVNGAKEPPPPVSA 226

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/6C_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	769	64.1	162	4	US-09-152-060-63
2	714	59.5	137	4	US-09-152-060-97
3	553.5	46.1	233	4	US-09-886-319A-12
4	541.5	45.1	233	4	US-09-886-319A-11
5	417	34.8	87	4	US-09-152-060-98
6	175.5	14.6	262	3	US-08-889-425-2
7	156	13.0	261	3	US-08-889-425-4
8	95	7.9	1872	6	5386025-6
9	95	7.9	1873	1	US-08-435-675B-4
10	95	7.9	1873	1	US-08-336-257A-7
11	89	7.4	713	4	US-09-107-532A-4559
12	88.5	7.4	2161	1	US-07-745-206A-2
13	88.5	7.4	2161	1	US-08-455-543A-49
14	88.5	7.4	2161	1	US-08-455-543A-51
15	88.5	7.4	2161	2	US-08-223-305C-49
16	88.5	7.4	2161	2	US-08-223-305C-51
17	88.5	7.4	2161	2	US-08-311-363-2
18	87.5	7.3	451	1	US-08-191-337-3
19	87.5	7.3	548	4	US-09-328-352-6605
20	86.5	7.2	241	4	US-09-107-532A-5558
21	85.5	7.1	667	3	US-08-959-004-11
22	83	6.9	775	4	US-09-252-991A-28461
23	83	6.9	870	4	US-09-134-001C-4959
24	82.5	6.9	493	3	US-08-476-123-12
25	80	6.7	315	4	US-09-393-634-56
26	80	6.7	1968	1	US-07-745-206A-7
27	80	6.7	1968	1	US-08-455-543A-45

28	80	6.7	1968	2	US-08-223-305C-45	Sequence 45, Appli
29	80	6.7	1968	2	US-08-311-363-7	Sequence 7, Appli
30	79.5	6.6	120	3	US-09-188-330-180	Sequence 180, App
31	79.5	6.6	120	4	US-09-312-283C-180	Sequence 180, App
32	79.5	6.6	421	4	US-09-198-452A-932	Sequence 932, App
33	79	6.6	219	2	US-08-855-140-3	Sequence 3, Appli
34	79	6.6	219	2	US-08-807-044-3	Sequence 3, Appli
35	79	6.6	219	5	PCT-US91-04986-2	Sequence 2, Appli
36	79	6.6	226	4	US-09-694-094-1	Sequence 1, Appli
37	78.5	6.5	907	1	US-08-349-006-2	Sequence 2, Appli
38	78.5	6.5	907	3	US-08-804-439A-19	Sequence 19, Appli
39	78.5	6.5	907	3	US-08-720-229-19	Sequence 19, Appli
40	78.5	6.5	907	4	US-09-171-699-2	Sequence 2, Appli
41	78.5	6.5	907	5	PCT-US94-04180-2	Sequence 2, Appli
42	77.5	6.5	358	4	US-08-937-834-4	Sequence 4, Appli
43	76.5	6.4	309	4	US-09-393-634-49	Sequence 49, Appli
44	76.5	6.4	344	4	US-09-134-001C-4175	Sequence 4175, Ap
45	76.5	6.4	373	4	US-09-252-991A-26370	Sequence 26370, A

ALIGNMENTS

RESULT 1
US-09-152-060-63
; Sequence 63, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-63

Query Match	64.1%;	Score 769;	DB 4;	Length 162;
Best Local Similarity	99.3%;	Pred. No. 7.8e-74;	Mismatches 1;	Indels 0;
Matches 146;	Conservative 0;			Gaps 0;
Qy	1	MKWVAPTRFYSNCCLCCHVTRCTILLGVYLLINAVLLILLSALADPPQYNFSSSEL	60	
Db	1	MKWVAPTRFYSNCCLCCHVTRCTILLGVYLLINAVLLILLSALADPPQYNFSSSEL	60	
Qy	61	GGDFEFDDNMCTIAISLMLICAMATYGAKQAAMIIFFCQIFDFALNMLVAI	120	
Db	61	GGDFEFDDNMCTIAISLMLICAMATYGAKQAAMIIFFCQIFDFALNMLVAI	120	

Qy 121 TVLIYPNSIQEYIRQLPPNPFYRDDVM 147
Db 121 TVLIYPNSIQEYIRQLPPNPFYRDDVM 147

RESULT 2
US-09-152-060-97
; Sequence 97, Application US/09152060,
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152.060
; EARLIER FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040.762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040.710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050.934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048.100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048.357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048.189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057.765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048.970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068.368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 97
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-97

Query Match 59.5%; Score 714; DB 4; Length 137;
Best Local Similarity 99.3%; Pred. No. 4.2e-68;
Matches 136; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 RFYNSCCLCHVRTGTLIGWVLIINAVVLLILLSALADPDQYNSSELGGDFEFD 68
Db 1 RFYNSCCLCHVRTGTLIGWVLIINAVVLLILLSALADPDQYNSSELGGDFEFD 60
Qy 69 DANMCIAIAISLLMLICAMATYGAAYKQRAAWIIPFCYQIFDFALNMLVAITVLIYPNS 128
Db 61 DANMCIAIAISLLMLICAMATYGAAYKQRAAGIIPFCYQIFDFALNMLVAITVLIYPNS 120
Qy 129 IQEYIRQLPPNPFYRDD 145
Db 121 IQEYIRQLPPNPFYRDD 137

RESULT 3
US-09-886-319A-12
; Sequence 12, Application US/09886319A
; Patent No. 6586185
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jorn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically

; TITLE OF INVENTION: Active Substances
; FILE REFERENCE: 50125/014002
; CURRENT APPLICATION NUMBER: US/09/886.319A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 10030149.5
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-319A-12
Query Match 46.1%; Score 553.5; DB 4; Length 233;
Best Local Similarity 45.2%; Pred. No. 7.8e-51;
Matches 104; Conservative 45; Mismatches 60; Indels 21; Gaps 6;
Qy 9 RFYNSCCLCHVRTGTLIGWVLIINAVVLLILLSALADPD-----QY-----NFSS 57
Db 13 RFYSTRCCGCHVRTGTLIGTWVNVLLMAILLTVETVTHPNSMPAVNIQYEVIGNYS 72
Qy 58 SELGGDFEFMDANMCIAIAISLLMLICAMATYGAAYKQRAAWIIPFCYQIFDFALNML 117
Db 73 SERMAD-----NACVLFASVLMFTISSMLVYGATSYQVGMWLIIPFCYRLEDFVLSCL 125
Qy 118 VAITVLIYPNSIQEYIRQLPPNPFYRDDVMSVNPCTCLVLIILFISILTPKGVLIISCVW 177
Db 126 VAISSTYLPRIKEYLDQL--PDFPYKDDLLALDSSCLLFVLVFFALFIIFKAYLINCVW 184
Qy 178 NCYRYINGRNSDVLVY-VTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 185 NCYKYNRRNVPEIANYPAEPQYVLYPYEMA-VKMPEKEPPPPYVLP 233

RESULT 4
US-09-886-319A-11
; Sequence 11, Application US/09886319A
; Patent No. 6586185
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jorn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
; TITLE OF INVENTION: Active Substances
; FILE REFERENCE: 50125/014002
; CURRENT APPLICATION NUMBER: US/09/886.319A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 10030149.5
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-886-319A-11

Query Match 45.1%; Score 541.5; DB 4; Length 233;
Best Local Similarity 44.8%; Pred. No. 1.5e-49;
Matches 103; Conservative 44; Mismatches 62; Indels 21; Gaps 6;
Qy 9 RFYNSCCLCHVRTGTLIGWVLIINAVVLLILLSALADPD-----QY-----NFSS 57
Db 13 RFYSTRCCGCHVRTGTLIGTWVNVLLMAILLTVETVTHPNSMPAVNIQYEVIGNYS 72

Qy 58 SELGGDFEFDANMCIAISLMLICAMATYGAYKQRAAWIIPFCYQIPFALNML 117
Db 73 SERMAD-----NACVLPAVSLMPTISSMLVYGAISQVGMILIPFCYRLDFVLSCL 125
Qy 118 VAITLVIPNSIQBYRQLPNPFYRDDVMSVNPCTLVLLILFISILITFKGYLISCVW 177
Db 126 VAISLTYLPRIKEYLQ-L-PDFPKDALLALDSSCLFVLVFEVVFVFIIFKAYLNCVW 184
Qy 178 NCYRYINGRSSDLVAV-VTSNDTTLVLLPPVDDATVNGAAKEPPPPVUSA 226.
Db 185 NCYKYNINNVPEIAVYAPETPPQYVLPITYEMA-VKIPKEPPPPVLPDA 233

RESULT 5

US-09-152-060-98
; Sequence 98, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1 US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 98
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-98

Query Match 34.8%; Score 417; DB 4; Length 87;
Best Local Similarity 92.0%; Pred. No. 6.4e-37;
Matches 80; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 140 PPRDDVMSVNPCTLVLLILFISILITFKGYLISCVWNCYRYINGRSSDLVYVTSND 199
Db 1 PPTEMSCAVNPCTLVLLILFISILITFKGYLISCVWNCYRYINGRSSDLVYVTSND 60
Qy 200 TTVLLPPVDDATVNGAAKEPPPPVUSA 226
Db 61 TTVLLPPVDDATVNGAAKEPPPPVUSA 87

RESULT 6

US-08-889-425-2
; Sequence 2, Application US/08889425
; Patent No. 6153403
; GENERAL INFORMATION:
; APPLICANT: Lim, Bing
; APPLICANT: Adra, Chaker N.
; TITLE OF INVENTION: A Lysosomal-Associated Multispanning

; TITLE OF INVENTION: Membrane Protein, LAPTMS and a Nucleic Acid Encoding
; TITLE OF INVENTION: LAPTMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,425
; FILING DATE: 08-JUL-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: BIH96-09pa
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 262 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-889-425-2

Query Match 14.8%; Score 175.5; DB 3; Length 262;
Best Local Similarity 22.8%; Pred. No. 9.1e-11;

Matches 61; Conservative 48; Mismatches 83; Indels 75; Gaps 12;
Qy 14 SCCLCCHVGTGILLGVWLLINAVLLILLALADPDQVNFSSSELGGDFEFMDANMC 73
Db 11 TCC-CFNVRIATTAIAHYVIM-SVLLFIEHSEVAGKASCKUSQMG----YLRIDALI 64
Qy 74 IATAISLLMILICAMATYGAYKQRAAWIIPFCYQIPFDFALNMLVAITLVIPNSIOEYI 133
Db 65 SSFLLITMLFIISLLIGVGNREKYLFLPSIQIMDYLCLLTLAGSYI---ELPAYL 121
Qy 134 -----ROLPPNPPYR-----DDVMSVNPCT----- 153
Db 122 KLASRSRASSSKFPLMTQLLDLFCLSILTLCSSYMEVPTYLNFKSMNMNYLPSQEDMPH 181
Qy 154 -----LVLILLFISILITFKGYLISCVWNCYRYINGRNS-----SDVLVYVTSNDTT 201
Db 182 NQFKOMIIFSIAPITVLI-FKVMFKCVWRCTRLIKMNSVEBKRSKML-----QK 233
Qy 202 VLLPPYDDATVNGAAKEP-----PPPY 223
Db 234 VLPSYEAA-LSLPSKTPEGGRAPPY 259

RESULT 7

US-08-889-425-4
; Sequence 4, Application US/08889425
; Patent No. 6153403
; GENERAL INFORMATION:
; APPLICANT: Lim, Bing
; APPLICANT: Adra, Chaker N.

; TITLE OF INVENTION: A Lysosomal-Associated Multispanning
; TITLE OF INVENTION: Membrane Protein, LAPTMS and a Nucleic Acid Encoding
; TITLE OF INVENTION: LAPTMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive

		Query Match	7.9%	Score 95;	DB 1;	Length 1873;	
		Best Local Similarity	24.0%;	Pred.No. 0.35,			
		Matches	46;	Conservative 31;	Mismatches 69;	Indels 46;	Gaps 9;

Qy	12	SNSCCLCHVRTGTILGVVLIINAVVLILLSALA----	DPOYNFSSSELGGDPEFM	67
	:	:	:	:
	:	:	:	:
	:	:	:	:
	:	:	:	:
Db	785	TNKVRVLCH---RIVNATWF--TNFILLPILLSAALAEADPIRAESVRNQILGYED--	836	

Qy	68	DDANMCTAIASLLMLILICAMATTGAYKQRAWTIIPFCYQIFDFALNMNLVAITVLVYPN	127	
	:	:	:	:
	:	:	:	:
	:	:	:	:
	:	:	:	:
Db	837	-----IAFTSVTFVEIVLKMTTGAFLHKS-----FCRNRYFNI-DLIIIVAVSLI---	881	

```

Query Match      7.4%; Score 89; DB 4; Length 713;
Best Local Similarity 21.0%; Pred. No. 0.45;
Matches "52; Conservative 38; Mismatches 80; Indels 68; Gaps 12;

Qy 26 ILGWVLIINAVVLIILISALADPOYNFSSE-----LG-GDFEFWDDANMCTAIA 77
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 187 IVLVICYLSFIVITII-----FAPSKMKETLKKMLGYNSPDTIKDSIKELNLL 237

Qy 78 ISLMILICAMATYGAYKQRAWIIFFCQIQIIFDFALNML-VAITVLVLYP-NSIQEYIRQ 135
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 238 FCSLIITFIILSIFLSIYVSNENFFLGLLCSIFHFIISFIVTIVSIYHLSSTIKNYLKN 297
   |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

```

Qy 136 LPPNFPYRDDVMSVNPCTCLVLIILLFISIIITFKGYLISCV-----W-- 177
Db 298 SRP-----LKLN--LCILNICLFLSMIL-----LJIASTKVNIHNEAENNSLKYWER 343
Qy 178 --NCR-----YINGRN-----SSVLVVTSTNDTTLVLPYDDATVNGAAKE 218
Db 344 TTNLKYKTNITQLNRNNTVBENNYLKKASKFPVYKIQNKYTFIIAPYNYATIQENNKE 401

RESULT 12
US-07-745-206A-2
; Sequence 2, Application US/07745206A
; Patent No. 5429921
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann
; APPLICANT: Feldman, Daniel
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Plannery
; STREET: 135 S. LaSalle
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/745.206A
; FILING DATE: 19910815
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feder, Scott B
; REFERENCE/DOCKET NUMBER: 51504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-372-7842
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-745-206A-2

Query Match 7.4%; Score 88.5; DB 1; Length 2161;
Best Local Similarity 25.0%; Pred. No. 2;
Matches 46; Conservative 34; Mismatches 61; Indels 43; Gaps 10;

Qy 21 VRTGILLGVWVLIINAVLILLSALA-----DP-DQYNFSSSELG-GDREFMDANCI 74
Db 875 IRVCGKLNHIFTNLVFMUSSAALAEEDPIRSHSFNTILGFYDFYAF----- 926
Qy 75 AIAISLLMILICAMATYGAKRAWIIPFCYQIFDPALNMLVAITVIYIPNSIOEYIR 134
Db 927 -TAIFTVEILL-KMTTFGAPLHKA-----FCRNVFNL-LDMLVVGSLV----- 968
Qy 135 QLPNFPYRDDVMSVNPCTCLVLIILLFISIIITFKG--YLISCVNVCYRYINGRNSDVL 192
Db 969 ----SFGIQSSAISVKILRLVRLPLRAINRAKGLKHVVQCQVFVAIRTI-----GNIM 1019
Qy 193 VYVT 196
Db 1020 IVTT 1023

RESULT 13

US-08-455-543A-49
; Sequence 49, Application US/08455543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,543A
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/223,305
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-52517
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-455-543A-49

Query Match 7.4%; Score 88.5; DB 1; Length 2161;
Best Local Similarity 25.0%; Pred. No. 2;
Matches 46; Conservative 34; Mismatches 61; Indels 43; Gaps 10;


```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seigman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-223-305C-49

```

```

Query Match      7.4%; Score 88.5; DB 2; Length 2161;
Best Local Similarity 25.0%; Pred.No.2;
Matches 46; Conservative 34; Mismatches 61; Indels 43; Gaps 10;

Qy      21 VRTGTLILGWYLLINAVLLILLSALA----DP-DQYNFSSSELG-GDFEFMDANMCI 74
Db      875 IRVGHKLINHIFTNLILVFIMLSAALAEDEPIRSHSPNTILGYFDYAP----- 926

Qy      75 AIAISLLMILICAMATYGAVKQRAAWIIPFCYQIFDFALNMLVAITVLIYPNSIQEYIR 134
Db      927 -TAIFTVEILL-KMTTFGAPLHKA-----FCRNYFNL-LDMLVVGSLV----- 968

Qy      135 QLPPNFPYRDDVMSVNPTCLVLIILFISILTPKG--YLISCVMNCYRYINGRNSDVL 192
Db      969 ----SFGIQSSAISVVKILRVLRPLRLRAINRAKGLKHVVQCQVFVAIRTI-----GNIM 1019

Qy      193 VYVT 196
Db      1020 IVTT 1023

```

Search completed: February 2, 2004, 14:24:17
Job time : 24 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2004, 14:21:56 ; Search time 177 Seconds
(without alignments)
1161.817 Million cell updates/sec

Title: US-09-965-529-26
Perfect score: 1200
Sequence: 1 MKMVAPWTRFYSNCCLCCH.....YDDATVNGAAKEPPPPYVSA 226

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA Main: *
1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/1/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/1/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/1/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/1/paa/US089_COMB.pep.*
14: /cgn2_6/ptodata/1/paa/US090_COMB.pep.*
15: /cgn2_6/ptodata/1/paa/US091_COMB.pep.*
16: /cgn2_6/ptodata/1/paa/US092_COMB.pep.*
17: /cgn2_6/ptodata/1/paa/US093_COMB.pep.*
18: /cgn2_6/ptodata/1/paa/US094_COMB.pep.*
19: /cgn2_6/ptodata/1/paa/US095_COMB.pep.*
20: /cgn2_6/ptodata/1/paa/US096_COMB.pep.*
21: /cgn2_6/ptodata/1/paa/US097A_COMB.pep.*
22: /cgn2_6/ptodata/1/paa/US097B_COMB.pep.*
23: /cgn2_6/ptodata/1/paa/US098_COMB.pep.*
24: /cgn2_6/ptodata/1/paa/US099A_COMB.pep.*
25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep.*
26: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
28: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
29: /cgn2_6/ptodata/1/paa/US103_COMB.pep.*
30: /cgn2_6/ptodata/1/paa/US104_COMB.pep.*
31: /cgn2_6/ptodata/1/paa/US106_COMB.pep.*
32: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1200	100.0	226	1	PCT-US01-16450-1994
					Sequence 1994, Ap

2	1200	100.0	226	1	PCT-US01-16450A-1994
3	1200	100.0	226	18	US-09-488-725A-2720
4	1200	100.0	226	20	US-09-611-523-2
5	1200	100.0	226	20	US-09-641-377-412
6	1200	100.0	226	21	US-09-743-247A-92
7	1200	100.0	226	25	US-09-965-529-26
8	1200	100.0	226	25	US-09-969-680A-26
9	1200	100.0	226	26	US-10-069-034-26
10	1200	100.0	226	27	US-10-126-052A-381
11	1200	100.0	226	28	US-10-258-898A-2720
12	1200	100.0	226	28	US-10-264-237-1994
13	1200	100.0	226	28	US-10-286-897-2720
14	1200	100.0	226	29	US-10-305-278-2
15	1200	100.0	231	18	US-09-488-725A-6292
16	1200	100.0	231	28	US-10-258-898A-6292
17	1200	100.0	231	28	US-10-286-897-6292
18	1200	100.0	254	1	PCT-US02-19592-125
19	1200	100.0	254	27	US-10-177-488-125
20	1200	100.0	283	1	PCT-US01-42950-364
21	1200	100.0	283	1	PCT-US02-07826-175
22	1200	100.0	283	1	PCT-US02-19592-124
23	1200	100.0	283	1	PCT-US02-37431-99
24	1200	100.0	283	26	US-10-097-340-175
25	1200	100.0	283	27	US-10-177-488-124
26	1200	100.0	283	29	US-10-301-822-99
27	1200	100.0	283	30	US-10-416-993-364
28	892.5	74.4	301	1	PCT-US01-08656-6669
29	892.5	74.4	301	28	US-10-273-573-6669
30	769	64.1	162	23	US-09-852-659-63
31	769	64.1	162	23	US-09-852-659A-63
32	769	64.1	162	23	US-09-852-797-63
33	769	64.1	162	23	US-09-853-161-63
34	769	64.1	162	26	US-10-058-993-63
35	714	59.5	137	23	US-09-852-659-97
36	714	59.5	137	23	US-09-852-659A-97
37	714	59.5	137	23	US-09-852-797-97
38	714	59.5	137	23	US-09-853-161-97
39	714	59.5	137	26	US-10-058-993-97
40	682	56.8	157	20	US-09-673-840A-244
41	553.5	46.1	221	20	US-09-641-377-413
42	553.5	46.1	233	1	PCT-US01-16450-2149
43	553.5	46.1	233	1	PCT-US01-16450A-2149
44	553.5	46.1	233	28	US-10-264-237-2149
45	553.5	46.1	233	29	US-10-376-564-12

ALIGNMENTS

RESULT 1
PCT-US01-16450-1994
; Sequence 1994, Application PC/TUS0116450
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA131PCT
; CURRENT APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2820
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1994
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-16450-1994

Query Match 100.0%; Score 1200; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MKMVAPWTRFYSNCCLCCHVRTGILLGVWYLIINAVVLLILLSALADPDQYNSSEL 60

Db 1 MKWAPWTRFYSNCCCLCHVTRGTILLGVWYLIINAVLLILLSALADPDQYNFSSSEL 60
Qy 61 GGDPEFDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIYDFALNMLVAI 120
Db 61 GGDPEFDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIYDFALNMLVAI 120
Qy 121 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLILLLFISILITFKGYLISCVNVCY 180
Db 121 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLILLLFISILITFKGYLISCVNVCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 2

PCT-US01-16450A-1994
; Sequence 1994, Application PC/TUS0116450A
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA131PCT
; CURRENT APPLICATION NUMBER: PCT/US01/16450A
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2820
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1994
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-16450A-1994

Query Match 100.0%; Score 1200; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKWAPWTRFYSNCCCLCHVTRGTILLGVWYLIINAVLLILLSALADPDQYNFSSSEL 60
Db 1 MKWAPWTRFYSNCCCLCHVTRGTILLGVWYLIINAVLLILLSALADPDQYNFSSSEL 60
Qy 61 GGDPEFDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIYDFALNMLVAI 120
Db 61 GGDPEFDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIYDFALNMLVAI 120
Qy 121 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLILLLFISILITFKGYLISCVNVCY 180
Db 121 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLILLLFISILITFKGYLISCVNVCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 3

US-09-488-725A-2720
; Sequence 2720, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: PCT_Files_versions 1.0
; SEQ ID NO 2720
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2720

Query Match 100.0%; Score 1200; DB 18; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWAPWTRFYSNCCCLCHVTRGTILLGVWYLIINAVLLILLSALADPDQYNFSSSEL 60
Db 1 MKWAPWTRFYSNCCCLCHVTRGTILLGVWYLIINAVLLILLSALADPDQYNFSSSEL 60
Qy 61 GGDPEFDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIYDFALNMLVAI 120
Db 61 GGDPEFDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIYDFALNMLVAI 120
Qy 121 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLILLLFISILITFKGYLISCVNVCY 180
Db 121 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLILLLFISILITFKGYLISCVNVCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 4

US-09-611-523-2
; Sequence 2, Application US/09611523
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: KAWAI, YURI
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: HAYASHI, KOJI
; TITLE OF INVENTION: SECRETORY PROTEIN OR MEMBRANE PROTEIN
; FILE REFERENCE: 084335/0121
; CURRENT APPLICATION NUMBER: US/09/611,523
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: JP 1999-194179
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: JP 2000-118775
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183766
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/159,586
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/183,323
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 679
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-611-523-2

Query Match 100.0%; Score 1200; DB 20; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Db 1 MKWVAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Qy 61 GGDFFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDFFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Qy 121 TVLIYPSNIOEYIROLPPNFPYRDDVMSVNPCTCLVLIILLFISILITFKGYLISCWVNCY 180
Db 121 TVLIYPSNIOEYIROLPPNFPYRDDVMSVNPCTCLVLIILLFISILITFKGYLISCWVNCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226

RESULT 5
US-09-641-377-412
; Sequence 412, Application US/09641377
; GENERAL INFORMATION:
; APPLICANT: WIEMANN, STEFAN
; APPLICANT: GASSENHUBER, JOHANN
; APPLICANT: TAMPE, JENS
; TITLE OF INVENTION: HUMAN DNA SEQUENCES
; FILE REFERENCE: 087100/0106
; CURRENT APPLICATION NUMBER: US/09/641,377
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/149,499
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 60/156,503
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 1793
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 412
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-641-377-412

Query Match 100.0%; Score 1200; DB 20; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKWVAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Db 1 MKWVAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Qy 61 GGDFFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDFFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Qy 121 TVLIYPSNIOEYIROLPPNFPYRDDVMSVNPCTCLVLIILLFISILITFKGYLISCWVNCY 180
Db 121 TVLIYPSNIOEYIROLPPNFPYRDDVMSVNPCTCLVLIILLFISILITFKGYLISCWVNCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226

RESULT 6
US-09-743-247A-92
; Sequence 92, Application US/09743247A
; GENERAL INFORMATION:
; APPLICANT: Sagami Chemical Research Center; Protegene Inc.
; TITLE OF INVENTION: Human Proteins Having Hydrophobic Domains And DNAs Encoding These
; FILE REFERENCE: 1997.13300
; CURRENT APPLICATION NUMBER: US/09/743,247A
; CURRENT FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: JP 10-208820
; PRIOR FILING DATE: 1998-07-24

; PRIOR APPLICATION NUMBER: JP 10-224105
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: JP 10-238116
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: JP 10-254736
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: JP 10-275505
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: Windows 95 (Word 98)
; SEQ ID NO 92
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-743-247A-92

Query Match 100.0%; Score 1200; DB 21; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKWVAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Db 1 MKWVAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Qy 61 GGDFFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDFFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Qy 121 TVLIYPSNIOEYIROLPPNFPYRDDVMSVNPCTCLVLIILLFISILITFKGYLISCWVNCY 180
Db 121 TVLIYPSNIOEYIROLPPNFPYRDDVMSVNPCTCLVLIILLFISILITFKGYLISCWVNCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226

RESULT 7
US-09-965-529-26
; Sequence 26, Application US/09965529
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dyoung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PP-0731 USA
; CURRENT APPLICATION NUMBER: US/09/965,529
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 26
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 2795577CDI
US-09-965-529-26

Query Match 100.0%; Score 1200; DB 25; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKWVAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Db 1 MKWVAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60

Db 1 MKWVAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Qy 61 GGDPEFDDANMCIAISLMLILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120
Db 61 GGDPEFDDANMCIAISLMLILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120
Qy 121 TVLIYPSNIOEYIRQLPFPNPPYRDDVMSVNPCTCLVLILILFISILITFKGYLISCVWNCY 180
Db 121 TVLIYPSNIOEYIRQLPFPNPPYRDDVMSVNPCTCLVLILILFISILITFKGYLISCVWNCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 8

US-09-969-680A-26

; Sequence 26, Application US/09969680A

; GENERAL INFORMATION:

; APPLICANT: LAL, Preeti; YUE, Henry

; APPLICANT: TANG, Y. Tom; BANDMAN, Olga

; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda

; APPLICANT: BAUGHN, Mariah R.; LU, Dyung Aina M.

; APPLICANT: PATTERSON, Chandra

; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS

; FILE REFERENCE: PP-0731-1 USA

; CURRENT APPLICATION NUMBER: US/09/969,680A

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US00/22315

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/149,641

; PRIOR FILING DATE: 1999-08-17

; PRIOR APPLICATION NUMBER: 60/164,203

; PRIOR FILING DATE: 1999-11-09

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PERL Program

; SEQ ID NO 26

; LENGTH: 226

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No: 2795577CD1

US-09-969-680A-26

Query Match 100.0%; Score 1200; DB 25; Length 226;

Best Local Similarity 100.0%; Pred. No. 4.8e-111;

Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Db 1 MKWVAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Qy 61 GGDPEFDDANMCIAISLMLILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120
Db 61 GGDPEFDDANMCIAISLMLILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120
Qy 121 TVLIYPSNIOEYIRQLPFPNPPYRDDVMSVNPCTCLVLILILFISILITFKGYLISCVWNCY 180
Db 121 TVLIYPSNIOEYIRQLPFPNPPYRDDVMSVNPCTCLVLILILFISILITFKGYLISCVWNCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 9

US-10-069-034-26

; Sequence 26, Application US/10069034

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: LAL, Preeti

; APPLICANT: YUE, Henry

; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PP-0731 PCT
; CURRENT APPLICATION NUMBER: US/10/069,034
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203
; PRIOR FILING DATE: 1999-08-17; 1999-11-09
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 26
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 2795577CD1
US-10-069-034-26

Query Match 100.0%; Score 1200; DB 26; Length 226;

Best Local Similarity 100.0%; Pred. No. 4.8e-111;

Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Db 1 MKWVAPWTRFYNSCCCHVTRGTILLGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Qy 61 GGDPEFDDANMCIAISLMLILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120
Db 61 GGDPEFDDANMCIAISLMLILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120
Qy 121 TVLIYPSNIOEYIRQLPFPNPPYRDDVMSVNPCTCLVLILILFISILITFKGYLISCVWNCY 180
Db 121 TVLIYPSNIOEYIRQLPFPNPPYRDDVMSVNPCTCLVLILILFISILITFKGYLISCVWNCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 10

US-10-126-052A-381

; Sequence 381, Application US/10126052A

; GENERAL INFORMATION:

; APPLICANT: Aziz, Natasha

; APPLICANT: Murray, Richard

; APPLICANT: Eos Biotechnology, Inc.

; TITLE OF INVENTION: Methods of Diagnosis of Lung Cancer, Compositions and

; FILE REFERENCE: 018501-001530US

; CURRENT APPLICATION NUMBER: US/10/126,052A

; CURRENT FILING DATE: 2002-04-18

; PRIOR APPLICATION NUMBER: US 60/284,770

; PRIOR FILING DATE: 2001-04-18

; PRIOR APPLICATION NUMBER: US 60/290,492

; PRIOR FILING DATE: 2001-05-10

; PRIOR APPLICATION NUMBER: US 60/339,245

; PRIOR FILING DATE: 2001-11-09

; PRIOR APPLICATION NUMBER: US 60/350,666

; PRIOR FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: US 60/334,370

; PRIOR FILING DATE: 2001-11-29

; PRIOR APPLICATION NUMBER: US 60/372,246

; NUMBER OF SEQ ID NOS: 691

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 381

; LENGTH: 226

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-126-052A-381

Query Match      100.0%; Score 1200; DB 27; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWAPWTRFYNSCCCLCHVTRGTILLGVWYLIINAVLLILLSALADPPQYNFSSSEL 60
Db 1 MKWAPWTRFYNSCCCLCHVTRGTILLGVWYLIINAVLLILLSALADPPQYNFSSSEL 60

Qy 61 GGDPEFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDPEFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120

Qy 121 TVLIYPNSIQEYIRQLPNFPYRDDVMSVNPCTCLVLIILLFISILTFKGYLISCVWNCY 180
Db 121 TVLIYPNSIQEYIRQLPNFPYRDDVMSVNPCTCLVLIILLFISILTFKGYLISCVWNCY 180

Qy 181 RYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 11
US-10-258-898A-2720
; Sequence 2720, Application US/10258898A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/10/258,898A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7143
; SOFTWARE: pf_fl_genes_b Versions 1.0
; SEQ ID NO 2720
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-898A-2720

Query Match      100.0%; Score 1200; DB 28; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWAPWTRFYNSCCCLCHVTRGTILLGVWYLIINAVLLILLSALADPPQYNFSSSEL 60
Db 1 MKWAPWTRFYNSCCCLCHVTRGTILLGVWYLIINAVLLILLSALADPPQYNFSSSEL 60

Qy 61 GGDPEFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDPEFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120

Qy 121 TVLIYPNSIQEYIRQLPNFPYRDDVMSVNPCTCLVLIILLFISILTFKGYLISCVWNCY 180
Db 121 TVLIYPNSIQEYIRQLPNFPYRDDVMSVNPCTCLVLIILLFISILTFKGYLISCVWNCY 180

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-1994
; Sequence 1994, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAI31P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1994
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-1994

Query Match      100.0%; Score 1200; DB 28; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWAPWTRFYNSCCCLCHVTRGTILLGVWYLIINAVLLILLSALADPPQYNFSSSEL 60
Db 1 MKWAPWTRFYNSCCCLCHVTRGTILLGVWYLIINAVLLILLSALADPPQYNFSSSEL 60

Qy 61 GGDPEFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDPEFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120

Qy 121 TVLIYPNSIQEYIRQLPNFPYRDDVMSVNPCTCLVLIILLFISILTFKGYLISCVWNCY 180
Db 121 TVLIYPNSIQEYIRQLPNFPYRDDVMSVNPCTCLVLIILLFISILTFKGYLISCVWNCY 180

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-897-2720
; Sequence 2720, Application US/10286897
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/10/286,897
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US/09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US/09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US/09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US/09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US/09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US/09/727,344
; PRIOR FILING DATE: 2000-11-29
```

```
; NUMBER OF SEQ ID NOS: 7143
; SOFTWARE: pt FL_genes_b Versions 1.0
; SEQ ID NO 2720
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-897-2720

Query Match      100.0%; Score 1200; DB 28; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYNSCCLCCHVRTGTTLLGVWYLIINAVVLLILLSALADPDQYNSSEL 60
Db 1 MKWVAPWTRFYNSCCLCCHVRTGTTLLGVWYLIINAVVLLILLSALADPDQYNSSEL 60

Qy 61 GGFDFWDDANMCIAIAISLLMILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120
Db 61 GGFDFWDDANMCIAIAISLLMILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120

Qy 121 TVLIYPNSIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
Db 121 TVLIYPNSIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt FL_genes_b Versions 1.0
; SEQ ID NO 6292
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-6292

Query Match      100.0%; Score 1200; DB 18; Length 231;
Best Local Similarity 100.0%; Pred. No. 4.9e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYNSCCLCCHVRTGTTLLGVWYLIINAVVLLILLSALADPDQYNSSEL 60
Db 6 MKWVAPWTRFYNSCCLCCHVRTGTTLLGVWYLIINAVVLLILLSALADPDQYNSSEL 65

Qy 61 GGFDFWDDANMCIAIAISLLMILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120
Db 66 GGFDFWDDANMCIAIAISLLMILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 125

Qy 121 TVLIYPNSIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
Db 126 TVLIYPNSIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 185

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 186 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 231

Search completed: February 2, 2004, 14:27:26
Job time : 179 secs

; NUMBER OF SEQ ID NOS: 7143
; SOFTWARE: pt FL_genes_b Versions 1.0
; SEQ ID NO 2720
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-897-2720

Query Match      100.0%; Score 1200; DB 28; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYNSCCLCCHVRTGTTLLGVWYLIINAVVLLILLSALADPDQYNSSEL 60
Db 1 MKWVAPWTRFYNSCCLCCHVRTGTTLLGVWYLIINAVVLLILLSALADPDQYNSSEL 60

Qy 61 GGFDFWDDANMCIAIAISLLMILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120
Db 61 GGFDFWDDANMCIAIAISLLMILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120

Qy 121 TVLIYPNSIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
Db 121 TVLIYPNSIOEYIRQLPPNPPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

; TITLE OF INVENTION: SECRETORY PROTEIN OR MEMBRANE PROTEIN
; FILE REFERENCE: 084335/0121
; CURRENT APPLICATION NUMBER: US/10/305,278
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US/09/611,523
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: JP 1999-194179
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: JP 2000-118775
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183766
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/159,586
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/183,323
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 679
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-305-278-2

Query Match      100.0%; Score 1200; DB 29; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.8e-111;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYNSCCLCCHVRTGTTLLGVWYLIINAVVLLILLSALADPDQYNSSEL 60
Db 1 MKWVAPWTRFYNSCCLCCHVRTGTTLLGVWYLIINAVVLLILLSALADPDQYNSSEL 60

Qy 61 GGFDFWDDANMCIAIAISLLMILICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAI 120
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2004, 14:22:31 ; Search time 24 Seconds
(without alignments)
724.790 Million cell updates/sec

Title: US-09-965-529-26
Perfect score: 1200
Sequence: 1 MKWVAPWTRFYSNCCCLCH.....YDDATVNGAAKEPPPPYVSA 226

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 370304 seqs, 76968869 residues

Total number of hits satisfying chosen parameters: 370304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Pending Patents AA New:*

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1200	100.0	283	6	US-10-734-564-97
2	1200	100.0	317	6	US-10-700-439-119
3	1181	98.4	234	1	PCT-US03-38808-248
4	1161	96.8	233	1	PCT-US03-38808-240
5	1144	95.3	319	1	PCT-US03-38808-241
6	282.5	23.5	425	5	US-09-614-150A-36129
7	282.5	23.5	432	5	US-09-614-150A-4479
8	175.5	14.6	262	1	PCT-US02-41798A-33
9	153	12.8	205	1	PCT-US03-37278-7
10	122	10.2	165	5	US-09-614-150A-42447
11	101	8.4	260	6	US-10-415-182A-4106
12	97.5	8.1	1772	6	US-10-726-216-16
13	95	7.9	1873	6	US-10-726-216-22
14	94	7.8	250	5	US-09-614-150A-207
15	91	7.6	551	6	US-10-679-063-24094
16	89	7.4	241	5	US-09-614-150A-30138
17	89	7.4	1633	1	PCT-US03-30720-722
18	88.5	7.4	1755	6	US-10-322-696A-51
19	88.5	7.4	1755	6	US-10-322-696B-51
20	88.5	7.4	2166	6	US-10-726-216-4
21	88.5	7.4	2181	5	US-09-976-858-288
22	88.5	7.4	2181	6	US-10-322-696A-54
23	88.5	7.4	2181	6	US-10-726-216-18
24	88.5	7.4	2181	6	US-10-726-216-20
25	88.5	7.4	2181	6	US-10-322-696B-54
26	88	7.3	537	6	US-10-679-063-23292

27 7.3 1543 1 PCT-US03-33087-52 Sequence 52, Appl
28 7.2 1787 6 US-10-357-885-30 Sequence 30, Appl
29 7.1 492 6 US-10-739-930-10011 Sequence 10011, A
30 6.9 507 6 US-10-679-063-13232 Sequence 13232, A
31 6.9 507 6 US-10-679-063-15216 Sequence 15216, A
32 6.9 1854 6 US-10-726-216-2 Sequence 2, Appl
33 6.9 1873 1 PCT-US03-38193-1433 Sequence 1433, Ap
34 6.9 1873 6 US-10-357-885-28 Sequence 28, Appl
35 6.9 1873 6 US-10-723-860-1433 Sequence 1433, Ap
36 6.9 1873 6 US-10-726-216-12 Sequence 12, Appl
37 6.9 1873 6 US-10-726-216-14 Sequence 14, Appl
38 6.8 223 5 US-09-614-150A-19326 Sequence 19326, A
39 6.8 359 6 US-10-330-773-930 Sequence 930, App
40 6.8 451 6 US-10-425-114A-47648 Sequence 47648, A
41 6.8 513 5 US-09-614-150A-23358 Sequence 23358, A
42 6.7 277 6 US-10-472-928-3476 Sequence 3476, Ap
43 6.7 314 7 US-60-500-315-1114 Sequence 1114, Ap
44 6.7 315 6 US-10-364-861-56 Sequence 56, Appl
45 6.7 380 6 US-10-343-650A-288 Sequence 288, App

ALIGNMENTS

RESULT 1

US-10-734-564-97

; Sequence 97, Application US/10734564

; GENERAL INFORMATION:

; APPLICANT: Christopher C Burgess et al

; TITLE OF INVENTION: Detection Methods Using TIMP1

; FILE REFERENCE: 1657/2012

; CURRENT APPLICATION NUMBER: US/10/734.564

; CURRENT FILING DATE: 2003-12-12

; NUMBER OF SEQ ID NOS: 138

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 97

; LENGTH: 283

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-734-564-97

Query Match 100.0%; Score 1200; DB 6; Length 283;

Best Local Similarity 100.0%; Pred. No. 2.1e-114;

Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKWVAPWTRFYSNCCCLCHVTRGTTLLGWYLIINAVLLILLSALADPPQYNSSEL	60
Db	58	MKWVAPWTRFYSNCCCLCHVTRGTTLLGWYLIINAVLLILLSALADPPQYNSSEL	117
Qy	61	GGDFEFDDANMCIAIAISLLMILICAMATYGAYKQRAAMIIPFCYQIFDFALNMLVAI	120
Db	118	GGDFEFDDANMCIAIAISLLMILICAMATYGAYKQRAAMIIPFCYQIFDFALNMLVAI	177
Qy	121	TVLIYPSNIEYIRQLPPNPFPYRDDVNSVNPCTLVLLILFISILITFKGVLISCVNVCY	180
Db	178	TVLIYPSNIEYIRQLPPNPFPYRDDVNSVNPCTLVLLILFISILITFKGVLISCVNVCY	237
Qy	181	RYINGRNSSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA	226
Db	238	RYINGRNSSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA	283

RESULT 2

US-10-700-439-119

; Sequence 119, Application US/10700439

; GENERAL INFORMATION:

; APPLICANT: Mayo Foundation for Medical Education and Research

; APPLICANT: Bayer Healthcare LLC

; APPLICANT: Burgess, Christopher

; APPLICANT: Myerow, Susan

; APPLICANT: Thiagalingam, Arunthathi

; APPLICANT: Maimonis, Peter

; APPLICANT: Molino, Gary

APPLICANT: Burtgart, Lawrence
APPLICANT: Boardman, Lisa A.
APPLICANT: Thibodeau, Steven
APPLICANT: Lewis, Marcia
TITLE OF INVENTION: Use of differentially Expressed Nucleic Acid Sequences as
FILE REFERENCE: 1657/2022
CURRENT APPLICATION NUMBER: US/10/700,439
CURRENT FILING DATE: 2003-11-04
NUMBER OF SEQ ID NOS: 186
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 119
LENGTH: 317
TYPE: PRT
ORGANISM: Homo sapiens
US-10-700-439-119

Query Match 100.0%; Score 1200; DB 6; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.4e-114;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKVAPWTRFYSNCCLCCHVRTGILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Db 92 MKVAPWTRFYSNCCLCCHVRTGILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 151
Qy 61 GGDFFEMDDANMCIAISLMLICAMATYGAYKQRAAWIIPFCYQIPDFALNMLVAI 120
Db 152 GGDFFEMDDANMCIAISLMLICAMATYGAYKQRAAWIIPFCYQIPDFALNMLVAI 211
Qy 121 TVLIYPNSIQEYIRQLPPNFPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
Db 212 TVLIYPNSIQEYIRQLPPNFPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 271
Qy 181 RYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 272 RYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA 317

RESULT 3
PCT-US03-38808-248
; Sequence 248, Application PC/TUS0338808
; GENERAL INFORMATION:
; APPLICANT: diadexus, Inc.
; APPLICANT: Macina, Roberto
; APPLICANT: Turner, Leah
; APPLICANT: Sun, Yongming
; APPLICANT: Rodriguez, Maria
; APPLICANT: Tim Burcham
; TITLE OF INVENTION: Compositions, Splice Variants and Methods Relating to Colon Spec
; FILE REFERENCE: DEX-0450
; CURRENT APPLICATION NUMBER: PCT/US03/38808
; CURRENT FILING DATE: 2003-12-04
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 248
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapien
PCT-US03-38808-248

Query Match 98.4%; Score 1181; DB 1; Length 234;
Best Local Similarity 96.2%; Pred. No. 1.5e-112;
Matches 225; Conservative 1; Mismatches 0; Indels 8; Gaps 1;
Qy 1 MKVAPWTRFYSNCCLCCHVRTGILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Db 1 MKVAPWTRFYSNCCLCCHVRTGILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Qy 61 GGDFFEMDDANMCIAISLMLICAMATYGAYKQRAAWIIPFCYQIPDF 112

Db 61 GGDFFEMDDAKILFNLSADMCIAISLMLICAMATYGAYKQRAAWIIPFCYQIPDF 120
Qy 113 ALANMLVAITVLIYPNSIQEYIRQLPPNFPYRDDVMSVNPCTCLVLIILFISILTFKGYL 172
Db 121 ALANMLVAITVLIYPNSIQEYIRQLPPNFPYRDDVMSVNPCTCLVLIILFISILTFKGYL 180
Qy 173 ISCVWNCYRYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 ISCVWNCYRYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA 234

RESULT 4
PCT-US03-38808-240
; Sequence 240, Application PC/TUS0338808
; GENERAL INFORMATION:
; APPLICANT: diadexus, Inc.
; APPLICANT: Macina, Roberto
; APPLICANT: Turner, Leah
; APPLICANT: Sun, Yongming
; APPLICANT: Rodriguez, Maria
; APPLICANT: Tim Burcham
; TITLE OF INVENTION: Compositions, Splice Variants and Methods Relating to Colon Spec
; FILE REFERENCE: DEX-0450
; CURRENT APPLICATION NUMBER: PCT/US03/38808
; CURRENT FILING DATE: 2003-12-04
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapien
PCT-US03-38808-240

Query Match 96.8%; Score 1161; DB 1; Length 233;
Best Local Similarity 97.8%; Pred. No. 1.6e-110;
Matches 219; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MKVAPWTRFYSNCCLCCHVRTGILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Db 1 MKVAPWTRFYSNCCLCCHVRTGILLGVWYLIINAVVLLILLSALADPPQYNFSSSEL 60
Qy 61 GGDFFEMDDANMCIAISLMLICAMATYGAYKQRAAWIIPFCYQIPDFALNMLVAI 120
Db 61 GGDFFEMDDANMCIAISLMLICAMATYGAYKQRAAWIIPFCYQIPDFALNMLVAI 120
Qy 121 TVLIYPNSIQEYIRQLPPNFPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
Db 121 TVLIYPNSIQEYIRQLPPNFPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYV 224
Db 181 RYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGACQCAPAYV 224

RESULT 5
PCT-US03-38808-241
; Sequence 241, Application PC/TUS0338808
; GENERAL INFORMATION:
; APPLICANT: diadexus, Inc.
; APPLICANT: Macina, Roberto
; APPLICANT: Turner, Leah
; APPLICANT: Sun, Yongming
; APPLICANT: Rodriguez, Maria
; APPLICANT: Tim Burcham
; TITLE OF INVENTION: Compositions, Splice Variants and Methods Relating to Colon Spec
; FILE REFERENCE: DEX-0450
; CURRENT APPLICATION NUMBER: PCT/US03/38808
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/431,133

;; PRIOR FILING DATE: 2002-12-04
;; NUMBER OF SEQ ID NOS: 254
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 241
;; LENGTH: 319
;; TYPE: PRT
;; ORGANISM: Homo sapien
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (2)..(5)
;; OTHER INFORMATION: Xeany amino acid
PCT-US03-38808-241

Query Match 95.3%; Score 1144; DB 1; Length 319;
Best Local Similarity 98.2%; Pred. No. 1.2e-108;
Matches 216; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKVAPWTRFYNSCCCLCHVRTGILLGVWYLIINAVVLLILSALADPDQYNFSSSEL 60
Db 85 MKVAPWTRFYNSCCCLCHVRTGILLGVWYLIINAVVLLILSALADPDQYNFSSSEL 144
Qy 61 GGFDFMDANNCIAISLMLILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAI 120
Db 145 GGFDFMDANNCIAISLMLILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAI 204
Qy 121 TVLIYPSNIOEYIRQLPFPYRDDVMSVNPCTCLVLIILFISILTPKGYLISCVWNCY 180
Db 205 TVLIYPSNIOEYIRQLPFPYRDDVMSVNPCTCLVLIILFISILTPKGYLISCVWNCY 264
Qy 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAKPEPP 220
Db 265 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGACQAP 304

RESULT 6

US-09-614-150A-36129
; Sequence 36129, Application US/09614150A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: DROSOPHILA GENES.

;; CURRENT APPLICATION NUMBER: US/09/614,150A
;; PRIOR FILING DATE: 2000-07-11
;; PRIOR APPLICATION NUMBER: 60/157,832
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: 60/160,191
;; PRIOR FILING DATE: 1999-10-19
;; PRIOR APPLICATION NUMBER: 60/161,932
;; PRIOR FILING DATE: 1999-10-28
;; PRIOR APPLICATION NUMBER: 60/164,769
;; PRIOR FILING DATE: 1999-11-12
;; PRIOR APPLICATION NUMBER: 60/173,383
;; PRIOR FILING DATE: 1999-12-28
;; PRIOR APPLICATION NUMBER: 60/175,693
;; PRIOR FILING DATE: 2000-01-12
;; PRIOR APPLICATION NUMBER: 60/184,831
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: 60/191,637
;; PRIOR FILING DATE: 2000-03-23
;; NUMBER OF SEQ ID NOS: 43008
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 36129
;; LENGTH: 425
;; TYPE: PRT
;; ORGANISM: DROSOPHILA
US-09-614-150A-36129

Query Match 23.5%; Score 282.5; DB 5; Length 425;
Best Local Similarity 26.4%; Pred. No. 9.2e-21;
Matches 68; Conservative 40; Mismatches 97; Indels 53; Gaps 5;

Qy 14 SCCLCCHVRTGILLGVWYLIINAVVLLILSALADPDQYNFSSSEL-GGDFEFMD-- 69
Db 32 TCCFGLVHTATLMIGLWHLFLNLALSVLAVIWRNPEMD-----ELEGGTHDVTDL 87
Qy 70 -----ANMCIAIAISLMLILICAMATYGAYKORAAWI 102
Db 88 PALPTPLSKVEPPYAYRDHSLNRYKRYQNFDMGLVCTCMIAITLMMIYGTIKGKPSHLL 147
Qy 103 PFCYQIFDFALNMLVAITVLIYPSNIOEYIRQLPFPYRDDVMSVNPCTCLVLIILF 162
Db 148 PFCYQIFDFALNMLVAITVLIYPSNIOEYIRQLPFPYRDDVMSVNPCTCLVLIILF 206
Qy 163 SIILTPKGYLISCVWNCYR-- 205
Db 207 ICIVFLKAYCIGIVMRCYKYLTLRQOHVTLFPPELPTGTVHSGVGGTGAERSYSTLLP 266
Qy 206 PYDDATVNGAKPEPPY 223
Db 267 NYDEAIAQYLKQAPPPSY 284

RESULT 7

US-09-614-150A-4479
; Sequence 4479, Application US/09614150A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: DROSOPHILA GENES.

;; CURRENT APPLICATION NUMBER: US/09/614,150A
;; PRIOR FILING DATE: 2000-07-11
;; PRIOR APPLICATION NUMBER: 60/157,832
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: 60/160,191
;; PRIOR FILING DATE: 1999-10-19
;; PRIOR APPLICATION NUMBER: 60/161,932
;; PRIOR FILING DATE: 1999-10-28
;; PRIOR APPLICATION NUMBER: 60/164,769
;; PRIOR FILING DATE: 1999-11-12
;; PRIOR APPLICATION NUMBER: 60/173,383
;; PRIOR FILING DATE: 1999-12-28
;; PRIOR APPLICATION NUMBER: 60/175,693
;; PRIOR FILING DATE: 2000-01-12
;; PRIOR APPLICATION NUMBER: 60/184,831
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: 60/191,637
;; PRIOR FILING DATE: 2000-03-23
;; NUMBER OF SEQ ID NOS: 43008
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 4479
;; LENGTH: 432
;; TYPE: PRT
;; ORGANISM: DROSOPHILA
US-09-614-150A-4479

Query Match 23.5%; Score 282.5; DB 5; Length 432;
Best Local Similarity 26.4%; Pred. No. 9.4e-21;
Matches 68; Conservative 40; Mismatches 97; Indels 53; Gaps 5;

Qy 14 SCCLCCHVRTGILLGVWYLIINAVVLLILSALADPDQYNFSSSEL-GGDFEFMD-- 69
Db 39 TCCFGLVHTATLMIGLWHLFLNLALSVLAVIWRNPEMD-----ELEGGTHDVTDL 94
Qy 70 -----ANMCIAIAISLMLILICAMATYGAYKORAAWI 102
Db 95 PALPTPLSKVEPPYAYRDHSLNRYKRYQNFDMGLVCTCMIAITLMMIYGTIKGKPSHLL 154
Qy 103 PFCYQIFDFALNMLVAITVLIYPSNIOEYIRQLPFPYRDDVMSVNPCTCLVLIILF 162
Db 155 PFCYQIFDFALNMLVAITVLIYPSNIOEYIRQLPFPYRDDVMSVNPCTCLVLIILF 213

Qy 163 SIILTFKYLISCWNCYRYI-----NGNSSDLVYVTSNDTTVLLP 205
Db 214 ICIVFLKAYCIGIVWCYKYLTLRQHVRLFPFLPEPTGVHSGGTGGAERYSYTLTP 273
Qy 206 PYDDATVNGAAKEPPPPY 223
Db 274 NYDEAIAQLKQAPPPSY 291

RESULT 8
PCT-US02-41798A-33
; Sequence 33, Application PC/TUS0241798A
; GENERAL INFORMATION:
; APPLICANT: FRANTZ, GRETCHEN
; APPLICANT: HILLAN, KENNETH J.
; APPLICANT: PHILLIPS, HEIDI S.
; APPLICANT: POLAKIS, PAUL
; APPLICANT: SMITH, VICTORIA
; APPLICANT: SPENCER, SUSAN D.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WU, THOMAS D.
; APPLICANT: ZHANG, ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/41798A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 33
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapien
PCT-US02-41798A-33

Query Match 14.6%; Score 175.5; DB 1; Length 262;
Best Local Similarity 22.8%; Pred. No. 4.2e-10;
Matches 61; Conservative 48; Mismatches 83; Indels 75; Gaps 12;
Qy 14 SCCLCCHVRTGTLIGVWYLIINAVVLLILLSALADPDQYNSFSSSELGGDFEFMDANMC 73
Db 11 TCC-CFNVRIATTALAIYHVIM-VSLFLFIEHSEVAGKASCKLSQMG-----YLRADLI 64
Qy 74 IATAISLMLICAMATYGAQKRAAWIIPFCYQIFDPALNMLVAITVLYPNISIOEYI 133
Db 65 SSFLITLMLFIISLLIGVVKNEKYLPLSLQIMDYLLCLTLGSGYI---ELPAYL 121
Qy 134 -----ROLPNFPYR-----DDVMSVNPCTC----- 153
Db 122 KLASRRASSKFFPLMTLQLDLFCLSILTLCSYMEVPTYLNFKSMNHVNLPSQEDMPH 181
Qy 154 -----LVLIITLLFISILTFKGYLISCWNCYRYNGNS-----SDVLVYVTSNDTT 201
Db 182 NQFIKMMIIFSIATITVLI-FKVTMFKCVMRCYRLIKCMNSVEEKRNSKML-----QK 233

Qy 202 VLLPPYDDATVNGAAKEP-----PPPY 223
Db 234 VVLPSYEEA-LSLPSKTPEGGPAPPY 259
RESULT 9
PCT-US03-37278-7
; Sequence 7, Application PC/TUS0337278
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; EMERLING, Brooke M.;
; APPLICANT: CHIEN, David; WANG, Jonathan T.;
; APPLICANT: RICHARDSON, Thomas W.; RAMKUMAR, Jayalaxmi;
; APPLICANT: KHARE, Reena; ELLIOTT, Vicki S.;
; APPLICANT: LEE, Soo Yeun; BHATIA, Umesh G.;
; APPLICANT: BURRILL, John D.; LEE, Sally;
; APPLICANT: BLAKE, Julie J.; HO, Anne;
; APPLICANT: ZHEN, Wenjin
; TITLE OF INVENTION: ORGANELLE-ASSOCIATED PROTEINS
; FILE REFERENCE: PF-1621 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/37278
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/429,445
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 60/430,833
; PRIOR FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7522328CDI
PCT-US03-37278-7
Query Match 12.8%; Score 153; DB 1; Length 205;
Best Local Similarity 22.1%; Pred. No. 6.1e-08;
Matches 53; Conservative 42; Mismatches 67; Indels 78; Gaps 12;
Qy 14 SCCLCCHVRTGTLIGVWYLIINAVVLLILLSALADPDQYNSFSSSELGGDFEFMDANMC 73
Db 11 TCC-CFNVRIATTALAIYHVNRKYLPL----- 39
Qy 74 IATAISLMLICAMATYGAQKRAAWI-----IPFCYQIFDPALNMLVA-- 119
Db 40 ---SLQIMDYLLCLTLGSGYIELPAYLKLASRRASSSKFFPLMTLQLDLFCLSILTLCS 96
Qy 120 --ITVLIYPN-SIQEYIROLP--PNFPYRDDVMSVNPCTCLVLIITLLFISILTFKGYLIS 174
Db 97 SYMEVPTYLNFKSMNHVNLPSQEDMPHNOFI-----KMMIIFSIATITVLI-FKVTMFK 150
Qy 175 CVWNCYRYINGNS-----SDVLVYVTSNDTTVLLPPYDDATVNGAAKEP-----PPPY 223
Db 151 CVWRCYRLIKCMNSVEEKRNSKML-----QKVLPSEYEA-LSLPSKTPEGGPAPPY 202
RESULT 10
US-09-614-150A-42447
; Sequence 42447, Application US/09614150A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/09/614,150A
; CURRENT FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19

```

; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42447
; LENGTH: 165
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-09-614-150A-42447

```

Query Match	10.2%	Score 122;	DB 5;	Length 165;
Best Local Similarity	21.7%;	Pred. No. 6.9e-05;		
Matches	40;	Conservative 42;	Mismatches 56;	Indels 46; Gaps 7;

Qy	13	NSCCLCCHVGTGTLGGVWYLIINAVLLIILLSALADPDQYNFSSSELGGDFEFMDD---	69
Db	7	NSCCLCOSTRNGSVISGILAVLSIIIVIFTT-----RVHFXTI-----IPDFIPNDIV	57
Qy	70	-----ANNCIAIAISLMLILICAMATGYAKORAAWIIPFCYQIFDPALNMLVAITVLI	124
Db	58	KIILVINLCMTILISLMLII-----GALKRNHYLMVPM-----VVLGIMIAIGLLI	103
Qy	125	YPNISQIEYIQLPNFPYRDDVMSPNPTCLVLI--LLPISILITFKGVLIISCVNVCYRYI	183
Db	104	-----SVIYTGIVFFIDGVLTGVLWMLFGLIVCAIMTYCWCVVYSEYANL	149
Qy	184	NGRN	187
		:	
Db	150	SEEN	153

```

RESULT 11
US-10-415-182A-4106
; Sequence 4106, Application US/10415182A
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/415.182A
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: GB-0028727.6
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12024
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 4106
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-10-415-182A-4106

```

```

Query Match      8.4%; Score 101; DB 6; Length 260;
Best Local Similarity 24.0%; Pred. No. 0.016;
Matches 41; Conservative 31; Mismatches 73; Indels 26; Gaps 6;

Qy 28 LGWYLIINAIVLL--ILLGALADPDQYNFSSSELGDPFEMDANMCIAIAISLLMLI 85
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 13 VGRWYLIINAIVLLSILGLV-----KALGNFS--TDTNSTSAQIFITILVLL 61

Qy 86 CAAWYTGAYKQRAAWIIPFFCYQIFDFALNMLVAITLVLYPNSI--QBYIRQLPENPFYR 143

```



```

; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 250
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-09-614-150A-207

Query Match 7.8%; Score 94; DB 5; Length 250;
Best Local Similarity 19.9%; Pred. No. 0.079;
Matches 45; Conservative 37; Mismatches 78; Indels 66; Gaps 10;

QY 3 MVAPWTRFVNSCCIL---CC-----HVRTGTILGGVWYLINAVVLLILLS 45
Db 1 MELPTVSGSAAACKWKNCRRSWEMLMAPVSPKNLRTTALLTSIYQLLIHSCALFLVLL 60
QY 46 ALADPDQ-----YNFSSSELGGDFEFMDNDANMCIAISLMLILICAM 88
Db 61 GLAHAEQMCVEULEDILDQKONGFYNM--SPFHNDLRLQTAQLAVATE-NLLYVMAGIA 117
QY 89 ATY-----GAYKORAAWIIPFCYQIFDFALNMLVAITVLIYPNSIQEYIROLPPN 139
Db 118 GYIALSATLFGVFNRPGLIIPWL---VVEFLL--MIGLGALVFWLRDTKIVQLLGGQ 172
QY 140 PFYRDDVMSVNPCTCLVLIILLFISILTF-KGYLISCWVNCYRYIN 184
Db 173 VFY-----FTICVILICMDYCKVWVMSFYQSLRTMN 204

RESULT 15
US-10-679-063-24094
; Sequence 24094, Application US/10679063
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52054)B
; CURRENT APPLICATION NUMBER: US/10/679,063
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: 60/415,758
; PRIOR FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 27373
; SEQ ID NO 24094
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-679-063-24094

Query Match 7.6%; Score 91; DB 6; Length 551;
Best Local Similarity 22.0%; Pred. No. 0.39;
Matches 37; Conservative 32; Mismatches 53; Indels 46; Gaps 9;

QY 22 RGTGTILGGVW-YLIINAVVLLILLSALADPDQYNFSSSELGGDFEFMDNDANMC-IAIAIS 79
Db 395 RSGTFLIAVTVAVLEIILNGLA-----SSTAIGAVF-----NVCTVALNVS 438
QY 80 LMLILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAITVLIYPNSIQEYIROLPPN 139
Db 439 YVPIILCKM-VYGR-MQKGFWMGKYSVWVNAPAVMTFMVAVTF----- 482
QY 140 PFYRDDVMSVNPCTCLVLIILLFISILTFKGYLISCWVNCYRYINGRN 187

```

Db 483 PPTRVPVTENNVAIVVFFVLILALVF-----W-----YTHGRH 518

Search completed: February 2, 2004, 14:28:02
Job time : 26 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	175.5	14.6	262	2	G02476	lysosomal-associat
2	102.5	8.5	250	2	T15415	hypothetical prote
3	99.5	8.3	672	2	S52673	probable membrane
4	98.5	8.2	265	2	T26217	hypothetical prote
5	96	8.0	151	2	T18949	hypothetical prote
6	95	7.9	308	2	T20043	hypothetical prote
7	95	7.9	1873	2	A30063	dihydropyridine re
8	94.5	7.9	240	2	T15785	hypothetical prote
9	93.5	7.8	301	2	T21308	hypothetical prote
10	92.5	7.7	275	2	A41786	probable sugar tra
11	91.5	7.6	1032	2	H87470	ABR2/AcrP/AcrF fam
12	91	7.6	343	2	T14245	NADH2 dehydrogenas
13	89	7.4	391	2	AH1762	hypothetical prote
14	88.5	7.4	1610	2	A46227	voltage-dependent
15	88.5	7.4	1646	2	JH0422	voltage-dependent
16	88.5	7.4	2161	2	AJ0564	calcium channel al
17	88.5	7.4	2181	2	S81198	calcium channel al
18	88.5	7.4	2203	2	T24742	voltage-dependent
19	88	7.3	372	2	T24392	voltage-dependent
20	88	7.3	440	2	E89921	hypothetical prote
21	87.5	7.3	309	2	T24804	hypothetical prote
22	87.5	7.3	470	2	S47892	neutral amino acid
23	87.5	7.3	562	2	T26242	hypothetical prote
24	87	7.2	295	2	T32202	hypothetical prote
25	87	7.2	639	2	T50793	hypothetical prote
26	87	7.2	2220	2	A45290	calcium channel pr
27	85.5	7.1	667	2	S64915	EMP70 protein prec
28	85.5	7.1	757	2	C89473	protein F52D2.7 li
29	85	7.1	254	2	T22339	hypothetical prote

A;Residues: 1-301 <W1>
A;Cross-references: EMBL:Z71186; PIDN:CAA94913.1; GSPDB:GN00028; CESP:F23D12.1
A;Experimental source: clone F23D12
C;Genetics:
A;Gene: CESP:F23D12.1
A;Map position: X
A;Introns: 55/1; 83/2; 109/3; 135/2; 181/3; 211/1; 225/3

Query Match 7.8%; Score 93.5; DB 2; Length 301;
Best Local Similarity 22.6%; Pred. No. 0.43;
Matches 38; Conservative 32; Mismatches 65; Indels 33; Gaps 6;
Qy 14 SCCLCCHVTRTGILLGVYLIINAVLLIL-----SALADPDQVNFSSSELGGDFEFMD 69
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
28 SC--CCHAKFTYIFIGFEITFCFLVAVLPDVTTRVCDKLSNDTSESLSFDHFEFENI 85
Qy 70 ANMCIAIAI-----SLMLICAMATYGAYKQRAAWIIPFCYQIFDPALMVLV 118
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
86 KNVAVSSFLCHNNIFCFWAIQILSVDMFYGIKTIREFWFFIPHEIFRIICLSLICLV 145
Qy 119 AITVLIYVNSIQEYIRQLPNFPYRDDVMS--VNPCTCLVILLIFISII 165
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
146 DAWLIFRAAS-----GTDDKWSYITP--IVIIAVAVGVI 178

RESULT 10

S41786
Probable sugar transport protein 2 - thermophilic bacterium RT8.B4
N;Alternate names: hypothetical protein 2
C;Species: thermophilic bacterium RT8.B4
C;Date: 07-Sep-1994 #sequence_revision 14-Feb-1997 #text_change 20-Aug-1999
C;Accession: S41786
R;Divided, P.P.; Gibbs, M.D.; Bergquist, P.L.
submitted to the EMBL Data Library, October 1993
A;Description: Cloning, sequencing and over expression of a multifunctional xylanase gene
A;Reference number: S41785
A;Accession: S41786
A;Molecule type: DNA
A;Residues: 1-275 <DNI>
A;Cross-references: EMBL:L18965; NID:g311185; PIDN:AA842042.1; PID:g311187
C;Superfamily: maltose transport protein malG

Query Match 7.7%; Score 92.5; DB 2; Length 275;
Best Local Similarity 22.3%; Pred. No. 0.49;
Matches 53; Conservative 33; Mismatches 69; Indels 83; Gaps 9;
Qy 26 ILGVVYLIINAVVLLILLSAL-----ADPDQVNFSSSELGGDFEFMDA 70
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
13 IFLAVVTLIADVPPELFMLFTSFKTQSELLSGNTWQIPRQPTIGNFSTVLEGNFTYL--K 70
Qy 71 NMCTAIAISLML-ICAMATYGAYKQRAAWIIPFCYQIFDFALN-----MLVA 119
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
71 NSVIAVSISVVLLIILISSMAA-----FAPSRKFAALNLLSLIAGNAIP 116
Qy 120 ITVLIYE-----NSIQ-----EYIRQLPNFPYRDDVMSV 149
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
117 IHVTLIPIYVLTNKLKYDTVPALIGPVVALSPMSIFILTEFWREIPLSEAAKIDGC 176
Qy 150 NPTCLVLIILFIS--IILTFKGYLISCVNVCYRNGRNSDVLVYVTSNDTTLVLP 205
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
177 SMFLYSDIILLPLSAPALITVGIYNGTYLWNEVF-----ALVLTSSPTRRTLP 225

RESULT 11

H87470
AcrB/AcrD/AcrF family protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H87470
R;Niernan, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonin, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: H87470
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1032 <STO>
A;Cross-references: GB:AE005673; NID:g13423218; PIDN:AAK23764.1; GSPDB:GN00148
C;Genetics:
A;Gene: CCL1788

Query Match 7.6%; Score 91.5; DB 2; Length 1032;
Best Local Similarity 24.4%; Pred. No. 2.1;
Matches 42; Conservative 21; Mismatches 72; Indels 37; Gaps 7;
Qy 59 ELGGDFEFMDANWCIAIAISLMLICAMATYGAYKQRAAWII-----PF 104
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
844 EMGGSIEEAGKANKALAVVFPFLFMVVIIFQVRSLSAMWVLLTAPLALGVAPTLL 903
Qy 105 FCYQIFDF-ALNMLVAITVLIYVNSI-----QEYIRQLPNFPY---RDDVMSVNPCTCLV 155
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
904 IFHQPFGNAILGLIALAGIIMNSLILGQIQINQEEGLDPHAVVEATVQARPVILT 963
Qy 156 LIILFISIIITFKGYLISCVN--CYRYNGRNSDVLVYVTSNDTTLVLP 205
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
964 ALAAVFAFIPLT-----LSVFSSMAYTLIGGTIGTIL-----TLVFLP 1003

RESULT 12

T14245
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - dermatophytic fungus (Trichophyton
C;Species: dermatophytic fungus Trichophyton rubrum
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C;Accession: T14245
R;de Bievre, C.; Dujon, B.
submitted to the EMBL Data Library, November 1998
A;Description: Organisation of the mitochondrial genome of Trichophyton rubrum, part III
A;Reference number: Z17938
A;Accession: T14245
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-343 <DEB>
A;Cross-references: EMBL:Y18476; PIDN:CAA77189.1
A;Experimental source: isolate IP 1817.89
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC3
A;Note: NADH1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 1
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 7.6%; Score 91; DB 2; Length 343;
Best Local Similarity 21.7%; Pred. No. 0.83;
Matches 47; Conservative 45; Mismatches 67; Indels 58; Gaps 12;
Qy 9 RFYSNCCCLCCHVTRTGILLG-----VWYLI-INAVVLLILLSALADPDQVNFSSSE 59
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
153 RFY-----ILLVILFTGSLNLTITTESQKVYFIFLPLPIFLIFFIGCIAETNAPDLAE 208
Qy 60 LGGDF--EFMDANWCIAIAISLL-----MILICAMAT---YGAYKQRAAWIIPFCYQI 109
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
209 AESELVSGFWTEHSVIFMIFFPFQAQVASIVLCILSLVFLGGYLN---ILPLNTYV 264
Qy 110 FDP-----ALANMLVAITVLIYVNSIQEYIRQLPNFPYRDDVMSVNPCTCLV 156
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
265 CDFNSLFSYDLINGLSLNLAKTAFILF---VFIVRASFPPIRF-DQLMSVCWTLLP 320
Qy 157 IILLFISIIITFKGYLISCVNVCYRYNGRNSDVLV 193
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
321 IITAYV-----VLLPCI-----VIGLSSILLI 343

RESULT 13

AH1762

```

Db      925  -TAFTVEILL-KMTTFGAFHLKGA-----FCRNYFNL-LDMLVVGSLV----- 966
Qy      135  QLPPNFPYRDDVMSVNPNTCLVLILLFISILITFKG--YLISCVWNCYRYINGRNSSDVL 192
Db      967  ----SFGIQSSAISVVKILRVLRPLRAINRAKGLKHVQCFFVAIRTI-----GNIM 1017
Qy      193  VYVT 196
Db      1018  IVTT 1021

RESULT 15
JH0422
voltage-dependent calcium channel complex alpha-1 chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 11-Jan-2000
C:Accession: JH0422; D35901; T60901
R:Hui, A.; Ellinor, P.T.; Krizanava, O.; Wang, J.J.; Diebold, R.J.; Schwartz, A.
R:Neuron 7, 35-44, 1991
A:Title: Molecular cloning of multiple subtypes of a novel rat brain isoform of
A:Reference number: JH0422; MUID:91299338; PMID:1648940
A:Accession: JH0422
A:Molecule type: mRNA
A:Residues: 1-1646 <HUI>
A:Cross-references: GB:M57682; NID:g206573; PIDN:AAA42015.1; PID:g206574
A:Experimental source: brain
R:Snutch, T.P.; Leonard, J.P.; Gilbert, M.M.; Lester, H.A.; Davidson, N.
R:Proc. Natl. Acad. Sci. U.S.A. 87, 3391-3395, 1990
A:Title: Rat brain expresses a heterogeneous family of calcium channels.
A:Reference number: A35901; MUID:90239020; PMID:16921134
A:Accession: D35901
A:Status: preliminary; nucleic acid sequence not shown; not compared with concen
A:Molecule type: mRNA
A:Residues: 1247-1434 <SNU>
A:Experimental source: brain
R:Yu, A.S.L.; Hebert, S.C.; Brenner, B.M.; Lytton, J.
R:Proc. Natl. Acad. Sci. U.S.A. 89, 10494-10498, 1992
A:Title: Molecular characterization and nephron distribution of a family of tra
A:Reference number: A46422; MUID:93066265; PMID:1279681
A:Accession: I60901
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1040-1261,1305-1365 <RES>
A:Cross-references: GB:M99221; NID:g203370; PIDN:AAA40895.1; PID:g203371
A:Experimental source: kidney
C:Comment: Calcium channels are essential for many cellular functions, such as
n.
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C:Keywords: alternative splicing; calcium binding; calcium channel; glycoprotein
F:1463-1491/Domain: calcium binding #status predicted <EFC>
F:1454, 224, 328/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:464, 848, 1489, 1584/Binding site: phosphate (Ser) (covalent) #status predicted
Query Match 7.4%; Score 88.5; DB 2; Length 1646;
Best Local Similarity 25.0%; Pred. No. 6.2;
Matches 46; Conservative

Qy      21  VRGTILLGWYLIINAVLILLISALA----DP-DQYNFSSSELG-GDPEFMDANWCI 74
Db      874  IRVGCHKLINHHITNLILFIMLSSAALAEPIRSHSPRNTILGYDYAF----- 925
Qy      75  AIAISLLMILICAMATYGAKORAAWIIPFCYQIFDALNMLVAITVLIYPNSIQEYIR 134
Db      926  -TAFTVEILL-KMTTFGAFHLKGA-----FCRNYFNL-LDMLVVGSLV----- 967
Qy      135  QLPPNFPYRDDVMSVNPNTCLVLILLFISILITFKG--YLISCVWNCYRYINGRNSSDVL 192
Db      968  ----SFGIQSSAISVVKILRVLRPLRAINRAKGLKHVQCFFVAIRTI-----GNIM 1018
Qy      193  VYVT 196
Db      1019  IVTT 1022

```

Search completed: February 2, 2004, 14:23:44
Job time : 24 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2004, 14:16:30 ; Search time 18 Seconds
(without alignments)
590.446 Million cell updates/sec

Title: US-09-965-529-26

Perfect score: 1200

Sequence: 1 MKVAPWTRFYSNCCCLCH.....YDDATVNGAKEPPPPVYSA 226

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553.5	46.1	233	1 MTRP_HUMAN	Q15012 homo sapien
2	541.5	45.1	233	1 MTRP_MOUSE	Q60961 mus musculus
3	175.5	14.6	262	1 LAM5_HUMAN	Q13571 homo sapien
4	156	13.0	261	1 LAM5_MOUSE	Q61168 mus musculus
5	95	7.9	1873	1 CCAS_RABIT	P07293 oryctolagus
6	93	7.8	1146	1 CCAS_RAT	Q02485 rattus norv
7	92.5	7.7	275	1 YOR2_CALSR	P40980 caldicellul
8	91	7.6	343	1 NULM_TRIRU	Q92238 trichophyto
9	91	7.6	551	1 AAP2_NEUCR	O59942 neurospora
10	89	7.4	297	1 T2R4_MOUSE	Q91kt3 mus musculus
11	88.5	7.4	1610	1 CCAD_MESAU	Q95244 mesocricetu
12	88.5	7.4	2161	1 CCAD_HUMAN	Q01668 homo sapien
13	88.5	7.4	2203	1 CCAD_RAT	P27732 rattus norv
14	88	7.3	274	1 NULM_DROMA	P29867 drosophila
15	87.5	7.3	470	1 MTR_NEUCR	Q13936 homo sapien
16	87	7.2	2221	1 CCAC_HUMAN	P38680 neurospora
17	85.5	7.1	274	1 NULM_DROSE	P29868 drosophila
18	85.5	7.1	274	1 NULM_DROSE	P29869 drosophila
19	85.5	7.1	667	1 EN70_YEAST	P32802 saccharomyc
20	85	7.1	347	1 CB2R_MOUSE	P47936 mus musculus
21	83	6.9	247	1 Y124_NPVAC	P41679 autographa
22	83	6.9	1873	1 CCAS_HUMAN	Q13698 homo sapien
23	83	6.9	2139	1 CCAC_MOUSE	Q01815 mus musculus
24	82.5	6.9	210	1 Y143_CABEL	Q11071 caenorhabdi
25	82	6.8	313	1 O1C1_HUMAN	Q15619 homo sapien
26	81.5	6.8	567	1 NULM_HANWI	P48906 hansenula w
27	81	6.8	201	1 PSS_METJA	Q58609 methanococc
28	81	6.8	337	1 OPSX_MOUSE	Q35214 mus musculus
29	81	6.8	341	1 NULM_DROME	P03896 drosophila
30	81	6.8	344	1 NULM_CYACA	P48899 cyanidium c
31	80	6.7	369	1 NULM_ACACA	Q37381 acanthamoeb
32	80	6.7	738	1 NULM_LIGUV	Q951a3 ligustrum v
33	80	6.7	2171	1 CCAC_RABIT	P15381 oryctolagus

34	79.5	6.6	433	1 SECY_RICPR	Q92c85 rickettsia
35	79	6.6	219	1 CD53_HUMAN	P19397 homo sapien
36	79	6.6	238	1 T4S7_MOUSE	Q9ack3 mus musculus
37	79	6.6	830	1 YUG2_YEAST	P40367 saccharomyc
38	78.5	6.5	440	1 CAPE_STAAU	P39854 staphylococ
39	78.5	6.5	907	1 VGLB_HCMVT	P13201 human cytom
40	78	6.5	263	1 YFJD_ECOLI	P76599 escherichia
41	78	6.5	432	1 Y672_METUA	Q58086 methanococc
42	77.5	6.5	358	1 HOP1_CABEL	O02100 caenorhabdi
43	77.5	6.5	1675	1 CLH_RAT	P11442 rattus norv
44	77	6.4	379	1 CYB_PSECU	Q92y49 pseudochiro
45	77	6.4	1017	1 KCH4_RAT	Q9x1t9 rattus norv

ALIGNMENTS

RESULT 1
MTRP_HUMAN
ID MTRP_HUMAN STANDARD; PRT; 233 AA.
AC Q15012;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Lysosomal-associated transmembrane protein 4A (Golgi 4-transmembrane spanning transporter MTP).
DE LAPTMA4 OR MTRP OR KIAA0108.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=95308325; PubMed=7788527;
RA Nagase T., Miyajima N., Tanaka A., Sazuka T., Seki N., Sato S., Tabata S., Ishikawa K.-I., Kawabayashi Y., Kotani H., Nomura N.;
RA "Prediction of the coding sequences of unidentified human genes. III. The coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by analysis of cDNA clones from human cell line KG-1.";
RT DNA Res. 2:37-43 (1995).
RL [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: MAY FUNCTION IN THE TRANSPORT OF NUCLEOSIDES AND/OR NUCLEOSIDE DERIVATIVES BETWEEN THE CYTOSOL AND THE LUMEN OF AN INTRACELLULAR MEMBRANE-BOUND COMPARTMENT (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MAY RESIDE IN AN INTRACELLULAR MEMBRANE-BOUND COMPARTMENT (POTENTIAL).
CC -!- DOMAIN: THE C-TERMINAL DOMAIN IS NECESSARY FOR RETENTION WITHIN INTRACELLULAR MEMBRANES (BY SIMILARITY).

Query Match 13.0%; Score 156; DB 1; Length 261;
Best Local Similarity 22.4%; Pred. No. 1.2e-06;
Matches 60; Conservative 48; Mismatches 82; Indels 78; Gaps 13;

Qy 14 SCCLCCHVTRTGILLGVYLLINAVLLILLSALADPDQYVNFSSSELGGDFEFMDANMC 73
Db 11 TCC-CFNRVATIALAIHVMS-VLLFIEHV-----EVARGKVSCEFMPYLRMA 61
Qy 74 IAIASLL---MILICAMATYGVKQRAWIIPFCYQIFDFAIMLVITVLYPNISIQ 130
Db 62 DLLSFLILGVLFITISLLGVVKNREKYLIPLSLQIMDFLLCLLTLGSIYI---ELP 118
Qy 131 EYIRQLPEN-FYRDDVMSVN--PTCLVLIILL-----160
Db 119 AYLKLARPRGSKVPLMTLQLLDFCLSSYMEVPTLYMFKSNHNVYLPDSQGV 178
Qy 161 ----FISILTF-----KGYLSVCWNCYRYINGRNSDVLVYVTSNDTT-----201
Db 179 PHSQFINMLIFSVAFITVLILKYMPKCVVTCYKFLKHNSA-----MEDSSSKMFL 231
Qy 202 -VLLPPYDDATVNGAAKEP-----PPPY 223
Db 232 KVALPSYEAA-LSLPKTPTEGDAPPY 258

RESULT 5
CCAS_RABIT
ID CCAS_RABIT STANDARD; PRT; 1873 AA.
AC P07293;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Voltage-dependent L-type calcium channel alpha-1S subunit (Calcium
channel, L type, alpha-1 polypeptide, isoform 3, skeletal muscle).
GN CACNA1S OR CACNA1.3 OR CACNA1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
(1)
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP TISSUE=Skeletal muscle;
RC MEDLINE=87258269; PubMed=3037387;
RA Tanabe T., Takeshima H., Mikami A., Flockerzi V., Takahashi H.,
RA Kangawa K., Kojima M., Matsuo H., Hirose T., Numa S.;
RT "Primary structure of the receptor for calcium channel blockers from
skeletal muscle.";
RL Nature 328:313-318(1987).
(2)
RN SEQUENCE FROM N.A.
RP TISSUE=Skeletal muscle;
RC MEDLINE=88336904; PubMed=2458626;
RA Ellis S.B., Williams M.E., Ways N.R., Brenner R., Sharp A.H.,
RA Leung A.T., Campbell K.P., McKenna E., Koch W.J., Hui A., Schwartz A.,
RA Harpold M.M.;
RT "Sequence and expression of mRNAs encoding the alpha 1 and alpha 2
subunits of a DHP-sensitive calcium channel.";
RL Science 241:1661-1664(1988).
(3)
RN BETA-SUBUNIT BINDING DOMAIN.
RP MEDLINE=94150724; PubMed=7509046;
RA Pragnell M., de Waard M., Mori Y., Tanabe T., Snutch T.P.,
RA Campbell K.P.;
RT "Calcium channel beta-subunit binds to a conserved motif in the I-II
cytoplasmic linker of the alpha 1-subunit.";
RL Nature 368:67-70(1994).
(4)
RN PHENYLALKYLAMINE-BINDING SITE.
RP MEDLINE=91067656; PubMed=2174553;
RA Striesnig J., Glossmann H., Catterall W.A.;
RT "Identification of a phenylalkylamine binding region within the alpha 1
subunit of skeletal muscle Ca2+ channels.";

Proc. Natl. Acad. Sci. U.S.A. 87:9108-9112(1990).
(5)
RN DIHYDROPYRIDINE-BINDING SITE.
RP MEDLINE=92010109; PubMed=1656465;
RX Nakayama H., Taki M., Striesnig J., Glossmann H., Catterall W.A.,
RA Kanaoka Y.;
RT "Identification of 1,4-dihydropyridine binding regions within the
alpha 1 subunit of skeletal muscle Ca2+ channels by photoaffinity
labeling with diazepam.";
RT Proc. Natl. Acad. Sci. U.S.A. 88:9203-9207(1991).
(6)
RN DIHYDROPYRIDINE-BINDING SITE.
RP MEDLINE=92073369; PubMed=1660150;
RX Striesnig J., Murphy B.J., Catterall W.A.;
RT "Dihydropyridine receptor of L-type Ca2+ channels: identification of
binding domains for [3H](+)-PN200-110 and [3H]azidopine within the
alpha 1 subunit.";
RT Proc. Natl. Acad. Sci. U.S.A. 88:10769-10773(1991).
(7)
RN PHOSPHORYLATION OF SER-687 AND SER-1617.
RP MEDLINE=89008420; PubMed=2844809;
RX Roehrkasten A., Meyer H.B., Nastainczyk W., Sieber M., Hofmann F.;
RT "CAMP-dependent protein kinase rapidly phosphorylates serine-687 of
the skeletal muscle receptor for calcium channel blockers.";
RL J. Biol. Chem. 263:15325-15329(1988).
(8)
RN PHOSPHORYLATION BY CAPK.
RP MEDLINE=89367340; PubMed=2549550;
RX Nunoki K., Florio V., Catterall W.A.;
RT "Activation of purified calcium channels by stoichiometric protein
phosphorylation.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:6816-6820(1989).
CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1S
GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE)
CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)
GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP), AND BY OMEGA-AGATOXIN-III
PHENYLALKYLAMINES, BENZOTHIAZEPINES, AND BY OMEGA-AGATOXIN-III
(OMEGA-AGA-III). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-
GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
CC CALCIUM CHANNELS CONTAINING THE ALPHA-1S SUBUNIT PLAY AN IMPORTANT
ROLE IN EXCITATION-CONTRACTION COUPLING IN SKELETAL MUSCLE.
CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY. AN
ADDITIONAL GAMMA SUBUNIT IS PRESENT ONLY IN SKELETAL MUSCLE L-TYPE
CHANNEL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: SKELETAL MUSCLE SPECIFIC.
CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC -1- DOMAIN: THE LOOP BETWEEN REPEATS II AND III INTERACTS WITH THE
RYANODINE RECEPTOR, AND IS THEREFORE IMPORTANT FOR CALCIUM RELEASE
FROM THE ENDOPLASMIC RETICULUM NECESSARY FOR MUSCLE CONTRACTION.
CC -1- PTM: THE ALPHA-1S SUBUNIT IS FOUND IN TWO ISOFORMS IN THE SKELETAL
MUSCLE: A MINOR FORM OF 212 KDA CONTAINING THE COMPLETE AMINO ACID
SEQUENCE, AND A MAJOR FORM OF 190 KDA DERIVED FROM THE FULL-LENGTH
FORM BY POST-TRANSLATIONAL PROTEOLYSIS CLOSE TO PHE-1690.
CC -1- PTM: BOTH THE MINOR AND MAJOR FORMS ARE PHOSPHORYLATED IN VITRO BY
CAPK. PHOSPHORYLATION BY CAPK STIMULATES THE CALCIUM CHANNEL
FUNCTION.
CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
FAMILY.

 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

EMBL; X05921; CAA29355.1; -;
 EMBL; M23919; AAA31159.1; -;
 PIR; A30063; A30063.
 PDB; 1DU1; 19-JUL-00.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002077; Ca channel.
 DR InterPro; IPR002111; Cat_channel_Trl.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR005446; LVDCALPHAI.
 DR InterPro; IPR005450; LVDCALPHAI.
 DR InterPro; IPR005820; M+channel_nlg.
 DR Pfam; PF00520; Ion_trans_4.
 DR PRINTS; PR00167; CACHANNEL.
 DR PRINTS; PR01630; LVDCALPHAI.
 DR PRINTS; PR01634; LVDCALPHAI.
 DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation; Polymorphism; 3D-structure.
 FT REPEAT 38 337
 FT REPEAT 418 664
 FT REPEAT 786 1068
 FT REPEAT 1105 1384
 FT DOMAIN 1 51
 FT TRANSMEM 52 70
 FT DOMAIN 71 88
 FT TRANSMEM 89 108
 FT DOMAIN 109 120
 FT TRANSMEM 121 139
 FT DOMAIN 140 160
 FT TRANSMEM 161 179
 FT DOMAIN 180 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 309
 FT TRANSMEM 310 334
 FT DOMAIN 335 432
 FT TRANSMEM 433 451
 FT DOMAIN 452 466
 FT TRANSMEM 467 486
 FT DOMAIN 487 494
 FT TRANSMEM 495 513
 FT DOMAIN 514 523
 FT TRANSMEM 524 542
 FT DOMAIN 543 561
 FT TRANSMEM 562 581
 FT DOMAIN 582 636
 FT TRANSMEM 637 661
 FT DOMAIN 662 799
 FT TRANSMEM 800 818
 FT DOMAIN 819 834
 FT TRANSMEM 835 854
 FT DOMAIN 855 866
 FT TRANSMEM 867 885
 FT DOMAIN 886 892
 FT TRANSMEM 893 911
 FT DOMAIN 912 930
 FT TRANSMEM 931 950
 FT DOMAIN 951 1040
 FT TRANSMEM 1041 1065
 FT DOMAIN 1066 1118
 FT TRANSMEM 1119 1137
 FT DOMAIN 1138 1152
 FT TRANSMEM 1153 1172
 FT DOMAIN 1173 1180
 FT TRANSMEM 1181 1199
 FT TRANSMEM 1199 1218
 FT TRANSMEM 1218 1237
 FT TRANSMEM 1237 1256
 FT TRANSMEM 1256 1275
 FT TRANSMEM 1275 1294
 FT TRANSMEM 1294 1313
 FT TRANSMEM 1313 1332
 FT TRANSMEM 1332 1351
 FT TRANSMEM 1351 1370
 FT TRANSMEM 1370 1389
 FT TRANSMEM 1389 1408
 FT TRANSMEM 1408 1427
 FT TRANSMEM 1427 1446
 FT TRANSMEM 1446 1465
 FT TRANSMEM 1465 1484
 FT TRANSMEM 1484 1503
 FT TRANSMEM 1503 1522
 FT TRANSMEM 1522 1541
 FT TRANSMEM 1541 1560
 FT TRANSMEM 1560 1579
 FT TRANSMEM 1579 1598
 FT TRANSMEM 1598 1617
 FT TRANSMEM 1617 1636
 FT TRANSMEM 1636 1655
 FT TRANSMEM 1655 1674
 FT TRANSMEM 1674 1693
 FT TRANSMEM 1693 1712
 FT TRANSMEM 1712 1731
 FT TRANSMEM 1731 1750
 FT TRANSMEM 1750 1769
 FT TRANSMEM 1769 1788
 FT TRANSMEM 1788 1807
 FT TRANSMEM 1807 1826
 FT TRANSMEM 1826 1845
 FT TRANSMEM 1845 1864
 FT TRANSMEM 1864 1883
 FT TRANSMEM 1883 1902
 FT TRANSMEM 1902 1921
 FT TRANSMEM 1921 1940
 FT TRANSMEM 1940 1959
 FT TRANSMEM 1959 1978
 FT TRANSMEM 1978 1997
 FT TRANSMEM 1997 2016
 FT TRANSMEM 2016 2035
 FT TRANSMEM 2035 2054
 FT TRANSMEM 2054 2073
 FT TRANSMEM 2073 2092
 FT TRANSMEM 2092 2111
 FT TRANSMEM 2111 2130
 FT TRANSMEM 2130 2149
 FT TRANSMEM 2149 2168
 FT TRANSMEM 2168 2187
 FT TRANSMEM 2187 2206
 FT TRANSMEM 2206 2225
 FT TRANSMEM 2225 2244
 FT TRANSMEM 2244 2263
 FT TRANSMEM 2263 2282
 FT TRANSMEM 2282 2301
 FT TRANSMEM 2301 2320
 FT TRANSMEM 2320 2339
 FT TRANSMEM 2339 2358
 FT TRANSMEM 2358 2377
 FT TRANSMEM 2377 2396
 FT TRANSMEM 2396 2415
 FT TRANSMEM 2415 2434
 FT TRANSMEM 2434 2453
 FT TRANSMEM 2453 2472
 FT TRANSMEM 2472 2491
 FT TRANSMEM 2491 2510
 FT TRANSMEM 2510 2529
 FT TRANSMEM 2529 2548
 FT TRANSMEM 2548 2567
 FT TRANSMEM 2567 2586
 FT TRANSMEM 2586 2605
 FT TRANSMEM 2605 2624
 FT TRANSMEM 2624 2643
 FT TRANSMEM 2643 2662
 FT TRANSMEM 2662 2681
 FT TRANSMEM 2681 2700
 FT TRANSMEM 2700 2719
 FT TRANSMEM 2719 2738
 FT TRANSMEM 2738 2757
 FT TRANSMEM 2757 2776
 FT TRANSMEM 2776 2795
 FT TRANSMEM 2795 2814
 FT TRANSMEM 2814 2833
 FT TRANSMEM 2833 2852
 FT TRANSMEM 2852 2871
 FT TRANSMEM 2871 2890
 FT TRANSMEM 2890 2909
 FT TRANSMEM 2909 2928
 FT TRANSMEM 2928 2947
 FT TRANSMEM 2947 2966
 FT TRANSMEM 2966 2985
 FT TRANSMEM 2985 3004
 FT TRANSMEM 3004 3023
 FT TRANSMEM 3023 3042
 FT TRANSMEM 3042 3061
 FT TRANSMEM 3061 3080
 FT TRANSMEM 3080 3099
 FT TRANSMEM 3099 3118
 FT TRANSMEM 3118 3137
 FT TRANSMEM 3137 3156
 FT TRANSMEM 3156 3175
 FT TRANSMEM 3175 3194
 FT TRANSMEM 3194 3213
 FT TRANSMEM 3213 3232
 FT TRANSMEM 3232 3251
 FT TRANSMEM 3251 3270
 FT TRANSMEM 3270 3289
 FT TRANSMEM 3289 3308
 FT TRANSMEM 3308 3327
 FT TRANSMEM 3327 3346
 FT TRANSMEM 3346 3365
 FT TRANSMEM 3365 3384
 FT TRANSMEM 3384 3403
 FT TRANSMEM 3403 3422
 FT TRANSMEM 3422 3441
 FT TRANSMEM 3441 3460
 FT TRANSMEM 3460 3479
 FT TRANSMEM 3479 3498
 FT TRANSMEM 3498 3517
 FT TRANSMEM 3517 3536
 FT TRANSMEM 3536 3555
 FT TRANSMEM 3555 3574
 FT TRANSMEM 3574 3593
 FT TRANSMEM 3593 3612
 FT TRANSMEM 3612 3631
 FT TRANSMEM 3631 3650
 FT TRANSMEM 3650 3669
 FT TRANSMEM 3669 3688
 FT TRANSMEM 3688 3707
 FT TRANSMEM 3707 3726
 FT TRANSMEM 3726 3745
 FT TRANSMEM 3745 3764
 FT TRANSMEM 3764 3783
 FT TRANSMEM 3783 3802
 FT TRANSMEM 3802 3821
 FT TRANSMEM 3821 3840
 FT TRANSMEM 3840 3859
 FT TRANSMEM 3859 3878
 FT TRANSMEM 3878 3897
 FT TRANSMEM 3897 3916
 FT TRANSMEM 3916 3935
 FT TRANSMEM 3935 3954
 FT TRANSMEM 3954 3973
 FT TRANSMEM 3973 3992
 FT TRANSMEM 3992 4011
 FT TRANSMEM 4011 4030
 FT TRANSMEM 4030 4049
 FT TRANSMEM 4049 4068
 FT TRANSMEM 4068 4087
 FT TRANSMEM 4087 4106
 FT TRANSMEM 4106 4125
 FT TRANSMEM 4125 4144
 FT TRANSMEM 4144 4163
 FT TRANSMEM 4163 4182
 FT TRANSMEM 4182 4201
 FT TRANSMEM 4201 4220
 FT TRANSMEM 4220 4239
 FT TRANSMEM 4239 4258
 FT TRANSMEM 4258 4277
 FT TRANSMEM 4277 4296
 FT TRANSMEM 4296 4315
 FT TRANSMEM 4315 4334
 FT TRANSMEM 4334 4353
 FT TRANSMEM 4353 4372
 FT TRANSMEM 4372 4391
 FT TRANSMEM 4391 4410
 FT TRANSMEM 4410 4429
 FT TRANSMEM 4429 4448
 FT TRANSMEM 4448 4467
 FT TRANSMEM 4467 4486
 FT TRANSMEM 4486 4505
 FT TRANSMEM 4505 4524
 FT TRANSMEM 4524 4543
 FT TRANSMEM 4543 4562
 FT TRANSMEM 4562 4581
 FT TRANSMEM 4581 4600
 FT TRANSMEM 4600 4619
 FT TRANSMEM 4619 4638
 FT TRANSMEM 4638 4657
 FT TRANSMEM 4657 4676
 FT TRANSMEM 4676 4695
 FT TRANSMEM 4695 4714
 FT TRANSMEM 4714 4733
 FT TRANSMEM 4733 4752
 FT TRANSMEM 4752 4771
 FT TRANSMEM 4771 4790
 FT TRANSMEM 4790 4809
 FT TRANSMEM 4809 4828
 FT TRANSMEM 4828 4847
 FT TRANSMEM 4847 4866
 FT TRANSMEM 4866 4885
 FT TRANSMEM 4885 4904
 FT TRANSMEM 4904 4923
 FT TRANSMEM 4923 4942
 FT TRANSMEM 4942 4961
 FT TRANSMEM 4961 4980
 FT TRANSMEM 4980 5000
 FT TRANSMEM 5000 5019
 FT TRANSMEM 5019 5038
 FT TRANSMEM 5038 5057
 FT TRANSMEM 5057 5076
 FT TRANSMEM 5076 5095
 FT TRANSMEM 5095 5114
 FT TRANSMEM 5114 5133
 FT TRANSMEM 5133 5152
 FT TRANSMEM 5152 5171
 FT TRANSMEM 5171 5190
 FT TRANSMEM 5190 5209
 FT TRANSMEM 5209 5228
 FT TRANSMEM 5228 5247
 FT TRANSMEM 5247 5266
 FT TRANSMEM 5266 5285
 FT TRANSMEM 5285 5304
 FT TRANSMEM 5304 5323
 FT TRANSMEM 5323 5342
 FT TRANSMEM 5342 5361
 FT TRANSMEM 5361 5380
 FT TRANSMEM 5380 5400
 FT TRANSMEM 5400 5419
 FT TRANSMEM 5419 5438
 FT TRANSMEM 5438 5457
 FT TRANSMEM 5457 5476
 FT TRANSMEM 5476 5495
 FT TRANSMEM 5495 5514
 FT TRANSMEM 5514 5533
 FT TRANSMEM 5533 5552
 FT TRANSMEM 5552 5571
 FT TRANSMEM 5571 5590
 FT TRANSMEM 5590 5609
 FT TRANSMEM 5609 5628
 FT TRANSMEM 5628 5647
 FT TRANSMEM 5647 5666
 FT TRANSMEM 5666 5685
 FT TRANSMEM 5685 5704
 FT TRANSMEM 5704 5723
 FT TRANSMEM 5723 5742
 FT TRANSMEM 5742 5761
 FT TRANSMEM 5761 5780
 FT TRANSMEM 5780 5800
 FT TRANSMEM 5800 5819
 FT TRANSMEM 5819 5838
 FT TRANSMEM 5838 5857
 FT TRANSMEM 5857 5876
 FT TRANSMEM 5876 5895
 FT TRANSMEM 5895 5914
 FT TRANSMEM 5914 5933
 FT TRANSMEM 5933 5952
 FT TRANSMEM 5952 5971
 FT TRANSMEM 5971 5990
 FT TRANSMEM 5990 6009
 FT TRANSMEM 6009 6028
 FT TRANSMEM 6028 6047
 FT TRANSMEM 6047 6066
 FT TRANSMEM 6066 6085
 FT TRANSMEM 6085 6104
 FT TRANSMEM 6104 6123
 FT TRANSMEM 6123 6142
 FT TRANSMEM 6142 6161
 FT TRANSMEM 6161 6180
 FT TRANSMEM 6180 6200
 FT TRANSMEM 6200 6219
 FT TRANSMEM 6219 6238
 FT TRANSMEM 6238 6257
 FT TRANSMEM 6257 6276
 FT TRANSMEM 6276 6295
 FT TRANSMEM 6295 6314
 FT TRANSMEM 6314 6333
 FT TRANSMEM 6333 6352
 FT TRANSMEM 6352 6371
 FT TRANSMEM 6371 6390
 FT TRANSMEM 6390 6409
 FT TRANSMEM 6409 6428
 FT TRANSMEM 6428 6447
 FT TRANSMEM 6447 6466
 FT TRANSMEM 6466 6485
 FT TRANSMEM 6485 6504
 FT TRANSMEM 6504 6523
 FT TRANSMEM 6523 6542
 FT TRANSMEM 6542 6561
 FT TRANSMEM 6561 6580
 FT TRANSMEM 6580 6600
 FT TRANSMEM 6600 6619
 FT TRANSMEM 6619 6638
 FT TRANSMEM 6638 6657
 FT TRANSMEM 6657 6676
 FT TRANSMEM 6676 6695
 FT TRANSMEM 6695 6714
 FT TRANSMEM 6714 6733
 FT TRANSMEM 6733 6752
 FT TRANSMEM 6752 6771
 FT TRANSMEM 6771 6790
 FT TRANSMEM 6790 6809
 FT TRANSMEM 6809 6828
 FT TRANSMEM 6828 6847
 FT TRANSMEM 6847 6866
 FT TRANSMEM 6866 6885
 FT TRANSMEM 6885 6904
 FT TRANSMEM 6904 6923
 FT TRANSMEM 6923 6942
 FT TRANSMEM 6942 6961
 FT TRANSMEM 6961 6980
 FT TRANSMEM 6980 7000
 FT TRANSMEM 7000 7019
 FT TRANSMEM 7019 7038
 FT TRANSMEM 7038 7057
 FT TRANSMEM 7057 7076
 FT TRANSMEM 7076 7095
 FT TRANSMEM 7095 7114
 FT TRANSMEM 7114 7133
 FT TRANSMEM 7133 7152
 FT TRANSMEM 7152 7171
 FT TRANSMEM 7171 7190
 FT TRANSMEM 7190 7209
 FT TRANSMEM 7209 7228
 FT TRANSMEM 7228 7247
 FT TRANSMEM 7247 7266
 FT TRANSMEM 7266 7285
 FT TRANSMEM 7285 7304
 FT TRANSMEM 7304 7323
 FT TRANSMEM 7323 7342
 FT TRANSMEM 7342 7361
 FT TRANSMEM 7361 7380
 FT TRANSMEM 7380 7400
 FT TRANSMEM 7400 7419
 FT TRANSMEM 7419 7438
 FT TRANSMEM 7438 7457
 FT TRANSMEM 7457 7476
 FT TRANSMEM 7476 7495
 FT TRANSMEM 7495 7514
 FT TRANSMEM 7514 7533
 FT TRANSMEM 7533 7552
 FT TRANSMEM 7552 7571
 FT TRANSMEM 7571 7590
 FT TRANSMEM 7590 7609
 FT TRANSMEM 7609 7628
 FT TRANSMEM 7628 7647
 FT TRANSMEM 7647 7666
 FT TRANSMEM 7666 7685
 FT TRANSMEM 7685 7704
 FT TRANSMEM 7704 7723
 FT TRANSMEM 7723 7742
 FT TRANSMEM 7742 7761
 FT TRANSMEM 7761 7780
 FT TRANSMEM 7780 7800
 FT TRANSMEM 7800 7819
 FT TRANSMEM 7819 7838
 FT TRANSMEM 7838 7857
 FT TRANSMEM 7857 7876
 FT TRANSMEM 7876 7895
 FT TRANSMEM 7895 7914
 FT TRANSMEM 7914 7933
 FT TRANSMEM 7933 7952
 FT TRANSMEM 7952 7971
 FT TRANSMEM 7971 7990
 FT TRANSMEM 7990 8009
 FT TRANSMEM 8009 8028
 FT TRANSMEM 8028 8047
 FT TRANSMEM 8047 8066
 FT TRANSMEM 8066 8085
 FT TRANSMEM 8085 8104
 FT TRANSMEM 8104 8123
 FT TRANSMEM 8123 8142
 FT TRANSMEM 8142 8161
 FT TRANSMEM 8161 8180
 FT TRANSMEM 8180 8200
 FT TRANSMEM 8200 8219
 FT TRANSMEM 8219 8238
 FT TRANSMEM 8238 8257
 FT TRANSMEM 8257 8276
 FT TRANSMEM 8276 8295
 FT TRANSMEM 8295 8314
 FT TRANSMEM 8314 8333
 FT TRANSMEM 8333 8352
 FT TRANSMEM 8352 8371
 FT TRANSMEM 8371 8390
 FT TRANSMEM 8390 8409
 FT TRANSMEM 8409 8428
 FT TRANSMEM 8428 8447
 FT TRANSMEM 8447 8466
 FT TRANSMEM 8466 8485
 FT TRANSMEM 8485 8504
 FT TRANSMEM 8504 8523
 FT TRANSMEM 8523 8542
 FT TRANSMEM 8542 8561
 FT TRANSMEM 8561 8580
 FT TRANSMEM 8580 8600
 FT TRANSMEM 8600 8619
 FT TRANSMEM 8619 8638
 FT TRANSMEM 8638 8657
 FT TRANSMEM 8657 8676
 FT TRANSMEM 8676 8695
 FT TRANSMEM 8695 8714
 FT TRANSMEM 8714 8733
 FT TRANSMEM 8733 8752
 FT TRANSMEM 8752 8771
 FT TRANSMEM 8771 8790
 FT TRANSMEM 8790 8809
 FT TRANSMEM 8809 8828
 FT TRANSMEM 8828 8847
 FT TRANSMEM 8847 8866
 FT TRANSMEM 8866 8885
 FT TRANSMEM 8885 8904
 FT TRANSMEM 8904 8923
 FT TRANSMEM 8923 8942
 FT TRANSMEM 8942 8961
 FT TRANSMEM 8961 8980
 FT TRANSMEM 8980 9000
 FT TRANSMEM 9000 9019
 FT TRANSMEM 9019 9038
 FT TRANSMEM 9038 9057
 FT TRANSMEM 9057 9076
 FT TRANSMEM 9076 9095
 FT TRANSMEM 9095 9114
 FT TRANSMEM 9114 9133
 FT TRANSMEM 9133 9152
 FT TRANSMEM 9152 9171
 FT TRANSMEM 9171 9190
 FT TRANSMEM 9190 9209
 FT TRANSMEM 9209 9228
 FT TRANSMEM 9228 9247
 FT TRANSMEM 9247 9266
 FT TRANSMEM 9266 9285
 FT TRANSMEM 9285 9304
 FT TRANSMEM 9304 9323
 FT TRANSMEM 9323 9342
 FT TRANSMEM 9342 9361
 FT TRANSMEM 9361 9380
 FT TRANSMEM 9380 9400
 FT TRANSMEM 9400 9419
 FT TRANSMEM 9419 9438
 FT TRANSMEM 9438 9457
 FT TRANSMEM 9457 9476
 FT TRANSMEM 9476 9495
 FT TRANSMEM 9495 9514
 FT TRANSMEM 9514 9533
 FT TRANSMEM 9533 9552
 FT TRANSMEM 9552 9571
 FT TRANSMEM 9571 9590
 FT TRANSMEM 9590 9609
 FT TRANSMEM 9609 9628
 FT TRANSMEM 9628 9647
 FT TRANSMEM 9647 9666
 FT TRANSMEM 9666 9685
 FT TRANSMEM 9685 9704
 FT TRANSMEM 9704 9723
 FT TRANSMEM 9723 9742
 FT TRANSMEM 9742 9761
 FT TRANSMEM 9761 9780
 FT TRANSMEM 9780 9800
 FT TRANSMEM 9800 9819
 FT TRANSMEM 9819 9838
 FT TRANSMEM 9838 9857
 FT TRANSMEM 9857 9876
 FT TRANSMEM 9876 9895
 FT TRANSMEM 9895 9914
 FT TRANSMEM 9914 9933
 FT TRANSMEM 9933 9952
 FT TRANSMEM 9952 9971
 FT TRANSMEM 9971 9990
 FT TRANSMEM 9990 10000

FT DOMAIN 1200 1231 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1232 1250 S4 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1251 1269 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1270 1289 S5 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1290 1356 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1357 1381 S6 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1382 1873 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1383 1873 BINDING TO THE BETA SUBUNIT.
 FT DOMAIN 357 374 POLY-LEU.
 FT TRANSMEM 375 568
 Query Match 7.9%; Score 95; DB 1; Length 1873;
 Best Local Similarity 24.0%; Pred. No. 1.8;
 Matches 46; Conservative 31; Mismatches 69; Indels 46; Gaps 9;
 Qy 12 SNSCCLCHVTRTGILLGVYLIINAVVLLILLSALA----DPQYNFSSSELGDPDFM 67
 Db 785 TNKRVVLCH----RIVNATWF--TNFILLILLSAALAEDPIRAESVRNQLGYFD-- 836
 Qy 68 DDANMCIAIAISLMILICAMATYQAYKQRAAWIIPFCYOIFDPALNMLVAITVLIYPN 127
 Db 837 -----IAFTSVFTVEIVKMTYGAFLHKS-----FCRNYFNI-LDLLVAVVSLI--- 881
 Qy 128 SIQYIRQLPFPYRDVMSVNPCLVLLILLIFISILITFKG--YLISCWNCVRYING 185
 Db 882 -----SMGLSSTISVVKILRVLRVLRPLRAINRAKGLKHVVQCVFAIRTIGN 930
 Qy 186 RNSSDVLVYVTS 197
 Db 931 -----IVLVT 936
 RESULT 6
 CCAS RAT STANDARD; PRT; 1146 AA.
 ID CCAS RAT STANDARD; PRT; 1146 AA.
 AC Q02485; P70484; Q01553; Q62817;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Voltage-dependent L-type calcium channel alpha-1s subunit (Calcium
 channel, L type, alpha-1 polypeptide, isoform 3, skeletal muscle)
 DE (ROB1) (Fragment).
 DE GN CACNA1S OR CACNA1A3 OR CACNA1 OR CACNA1 OR CCHLA3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCB1_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93122775; PubMed=1335956;
 RA Chin H., Krall M., Kim H.-L., Kozak C.A., Mock B.A.;
 RT "The gene for the alpha-1 subunit of the skeletal muscle
 RT dihydropyridine-sensitive calcium channel (Cchla3) maps to mouse
 RL chromosome 1.";
 RL Genomics 14:1089-1091 (1992).
 RN [2]
 RP SEQUENCE OF 597-691 FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93068265; PubMed=1279681;
 RA Yu A.S.-L., Hebert S.C., Brenner B.M., Lyttton J.;
 RT "Molecular characterization and nephron distribution of a family of
 RT transcripts encoding the pore-forming subunit of Ca2+ channels in the
 RT kidney.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10494-10498 (1992).
 RN [3]
 RP SEQUENCE OF 359-658 FROM N.A. (ISOFORM ROB1).
 RC TISSUE=Osteosarcoma;
 RX MEDLINE=96074617; PubMed=7479909;
 RA Barry B.L.R., Geseck P.A., Froehner S.C., Friedman P.A.;
 RT "Multiple calcium channel transcripts in rat osteosarcoma cells:
 RT selective activation of alpha 1D isoform by parathyroid hormone.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:10914-10918 (1995).
 RN [4]
 RP PHOSPHORYLATION BY CAPK.

RP SEQUENCE FROM N.A.
RX MEDLINE=97077616; PubMed=8920183;
RA Dwivedi P.P., Gibbs M.D., Saul D.J., Bergquist P.L.;
RT "Cloning, sequencing and overexpression in *Escherichia coli* of a
RT xylanase gene, xynA from the thermophilic bacterium Rt88.4 genus
RT *Caldicellulosiruptor*.";
RL Appl. Microbiol. Biotechnol. 45:96-93(1996).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM PERMEASE FAMILY. MALFG SUBFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L18965; AAB42042.1; -;
DR PIR; S41786; S41786.
DR InterPro; IPR000515; BPD transp.
DR Pfam; PF00528; BPD transp. 1.
DR PROSITE; PS00402; BPD_TRANS_PNN_MEMBER; 1.
KW Hypothetical protein; Transmembrane; Transport.
FT TRANSMEM 11 31
FT TRANSMEM 74 94 POTENTIAL.
FT TRANSMEM 108 128 POTENTIAL.
FT TRANSMEM 136 156 POTENTIAL.
FT TRANSMEM 185 205 POTENTIAL.
FT TRANSMEM 239 259 POTENTIAL.
SQ SEQUENCE 275 AA; 30857 MW; BD7A3246B4F50199 CRC64;

Query Match 7.7%; Score 92.5; DB 1; Length 275;
Best Local Similarity 22.3%; Pred. No. 0.44;
Matches 53; Conservative 33; Mismatches 69; Indels 83; Gaps 9;

Qy 26 ILLGVYLIINAVLLILLAL-----ADPQVNFSSSELGDFEFMDA 70
Db 13 IFLAVTLIADVPFLFMLEFTSFQTSLLSGNTQWIPQPTIGNFSTVLEGNFTYL--K 70

Qy 71 NNCIAISLLMIL-ICAMATYKAYKQRAAWIIPFCYQVDFPALN-----MLVA 119
Db 71 NSVAISIVSVLLIILSISSMAA-----FAPSRKFALNNLLYLIAGMAIP 116

Qy 120 ITVLIYP-----NSTQ-----EYIROLPPNPPYRDDVMSV 149
Db 117 IHVLIPIYVITNKILYDVTALIGPVVALSLPMSIFILTFKREIPELEEEAAKIDGC 176

Qy 150 NPTCLVLIILLFIS--IILTFKGLISCVNCRVINGRNSDVLVYVTSNDTTVLLP 205
Db 177 SMERLYSDILLPLSAPALITVGYNGTYLWNEFVF-----ALVITSPTRTTLP 225

RESULT 8
NUIUM TRIRU STANDARD; PRT; 343 AA.
AC Q92238;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 1 [EC 1.6.5.3].
GN ND1 OR NADH1.
OS Trichophyton rubrum.
OC Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Onygenales; Arthrodermataceae; mitosporic Arthrodermataceae;
OC Trichophyton.
OX NCBI_taxID=5551;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP 1817.89;
RX MEDLINE=99146870; PubMed=10022946;

de Bievre C., Dujon B.;
"Organisation of the mitochondrial genome of *Trichophyton rubrum* III.
DNA sequence analysis of the NADH dehydrogenase subunits 1, 2, 3, 4,
5 and the cytochrome b gene.";
Curr. Genet. 35:30-35(1999).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Y18476; CAA77189.1; -;
DR PIR; T14245; T14245.
DR InterPro; IPR001694; Resp_NADH_dhl.
DR Pfam; PF00146; NADHdh; 1.
DR PROSITE; PS00667; COMPLEX1_ND1_1; 1.
DR PROSITE; PS00668; COMPLEX1_ND1_2; 1.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
SQ SEQUENCE 343 AA; 38239 MW; D29CD3BF97CFED64 CRC64;

Query Match 7.6%; Score 91; DB 1; Length 343;
Best Local Similarity 21.7%; Pred. No. 0.74;
Matches 47; Conservative 45; Mismatches 67; Indels 58; Gaps 12;

Qy 9 RFVNSCCLCHVTRTGILG-----VWYLI-INAVLLILLALADPDQVNFSSSE 59
Db 153 RFY-----ILLVILFTGSLNLTITTESQKVVYVFLIPLFLIFPGICGTAEINRAFFDLAE 208

Qy 60 LGGDF--EFWDDANWCIAAISLL-----MLICAMAT---YGAYKQRAAWIIPFCYQI 109
Db 209 AESLVSGFMTEHSAVIFMIFFFLAQYASIVLICILSSVLFLGGYLN---ILPLNTYV 264

Qy 110 FDF-----ALNMLVAITVLIYPSIOEYIRQLPPNPPYRDDVMSVNPTCLVL 156
Db 265 CDFNSLPSDVLINGLSSLNLAIKTAFLIF---VPIWVASFPPIRF-DQLMSVCVTILLP 320

Qy 157 IILLFISIIITFKGLISCVNCRVINGRNSDVLV 193
Db 321 IITAYV-----VLLPCI-----VIGLNSILLI 343

RESULT 9
AAP2_NEUCR STANDARD; PRT; 551 AA.
ID AAP2_NEUCR
AC O59942;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Amino acid permease 2.
GN AAP-2 OR AAP2.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariales; Neurospora.
OX NCBI_taxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RL Margolles-Clark E., Bowman B.J.;
Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: Belongs to the amino acid permease family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC

```
CC EMBL; AF053231; AAC08355.1;
DR InterPro; IPR002293; AA/rel_permease.
DR InterPro; IPR004756; AA_permease.
DR InterPro; IPR004840; AA_permease.
DR InterPro; IPR004841; Permease.
DR PFAM; PF00324; aa_permeases; 1.
DR TIGRFAMs; TIGR00907; 2A0304; 1.
DR PROSITE; PS00218; AMINO ACID PERMEASE 1; 1.
KW Transport; Amino-acid transport; Transmembrane.
FT TRANSMEM 66 86 POTENTIAL.
FT TRANSMEM 90 110 POTENTIAL.
FT TRANSMEM 139 159 POTENTIAL.
FT TRANSMEM 188 208 POTENTIAL.
FT TRANSMEM 214 234 POTENTIAL.
FT TRANSMEM 255 275 POTENTIAL.
FT TRANSMEM 301 321 POTENTIAL.
FT TRANSMEM 347 367 POTENTIAL.
FT TRANSMEM 399 419 POTENTIAL.
FT TRANSMEM 424 444 POTENTIAL.
FT TRANSMEM 464 484 POTENTIAL.
FT TRANSMEM 496 516 POTENTIAL.
SQ SEQUENCE 551 AA; 59869 MW; C812C646B82F9ADF CRC64;

Query Match 7.6%; Score 91; DB 1; Length 551;
Best Local Similarity 22.0%; Pred. No. 1.2;
Matches 37; Conservative 32; Mismatches 53; Indels 46; Gaps 9;

Qy 22 RTGTILLGVW-YLINAVALVLLISALADPPQYNFSSSELGGDFEFDANWC-IAIAIS 79
Db 395 RSQTPLIAVTVYVLEIIINLGLA-----SSTAIGAVF-----NVCTVALNVS 438

Qy 80 LLMILICAMTYGAYKQRAAMIIFFCQVIFDFALNMLVAITLVLYPNSIQEYIRQLPPN 139
Db 439 YVPIPLCKM-VYGR-MQKGPWHMGKYSVWNAFVAVNTFWAVIFF----- 482

Qy 140 FPYRDDVMSVNPCTCLVAILLIFISILTFKGLYSCVWNCVRYINGRN 187
Db 483 FPTRVPTPENWYAVVFFVLLIALVF-----W-----YTHGRH 518

RESULT 10
ID2_R2R4_MOUSE STANDARD; PRT; 297 AA.
AC Q9JKT3;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE Taste receptor type 2 member 4 (T2R4) (Taste receptor type 2 member
DE 8) (T2R8)
GN TAS2R4 OR TAS2R8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND TOPOLOGY.
RC STRAIN=129/SvJ;
RX MEDLINE=20222571; PubMed=10761934;
RA Adler E., Hoon M.A., Mueller K.L., Chandrashekar J., Ryba N.J.P.,
RA Zuker C.S., Ryba N.J.;
RT "A novel family of mammalian taste receptors.";
RL Cell 100:693-702(2000).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=2022572; PubMed=10761935;
RA Chandrashekar J., Mueller K.L., Hoon M.A., Adler E., Feng L., Guo W.,
RA Zuker C.S., Ryba N.J.;
RT "T2R8 function as bitter taste receptors.";
RL Cell 100:703-711(2000).
RN [3]
RP REVIEW.
RX MEDLINE=22135574; PubMed=12139982;

RA Montmayeur J.-P., Matsunami H.;
RT "Receptors for bitter and sweet taste.";
RL Curr. Opin. Neurobiol. 12:366-371(2002).
RN [4]
RP REVIEW.
RX MEDLINE=21634924; PubMed=11696554;
RA Margolske R.F.;
RT "Molecular mechanisms of bitter and sweet taste transduction.";
RL J. Biol. Chem. 277:1-4(2002).
RN [5]
RP REVIEW.
RX MEDLINE=22469025; PubMed=12581520;
RA Zhang Y., Hoon M.A., Chandrashekar J., Mueller K.L., Cook B., Wu D.,
RA Zuker C.S., Ryba N.J.;
RT "Coding of sweet, bitter, and umami tastes: different receptor cells
RT sharing similar signaling pathways.";
RL Cell 112:293-301(2003).
CC -1- FUNCTION: Receptor that may play a role in the perception of
CC bitterness and is gustducin-linked. Activated by denatonium and
CC 6-n-propyl-2-thiouracil. May play a role in sensing the chemical
CC composition of the gastrointestinal content. The activity of this
CC receptor may stimulate alpha gustducin, mediate PLC-beta-2
CC activation and lead to the gating of TRPM5.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in subsets of taste receptor cells
CC of the tongue and palate epithelium and exclusively in gustducin-
CC positive cells. Expressed in 15% taste bud cells in circumvallate
CC and foliate papillae but only in 2% in fungiform papillae.
CC -1- MISCELLANEOUS: Most taste cells may be activated by a limited
CC number of bitter compounds; individual taste cells can
CC discriminate among bitter stimuli.
CC -1- SIMILARITY: Belongs to family T2R of G-protein coupled receptors.
CC -1- CAUTION: This protein was previously referred to T2R8, but due to
CC its high similarity towards the human T2R4 sequence it is
CC considered to be T2R4.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

EMBL; AF227148; AAF43921.1;
Pfam; PF05296; TAS2R; 1
Receptor; G-protein coupled receptor; Transmembrane.
DOMAIN 1 11 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 12 32 1 (POTENTIAL).
FT DOMAIN 33 46 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 47 67 2 (POTENTIAL).
FT DOMAIN 68 80 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 81 101 3 (POTENTIAL).
FT DOMAIN 102 128 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 129 149 4 (POTENTIAL).
FT DOMAIN 150 171 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 172 192 5 (POTENTIAL).
FT DOMAIN 193 229 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 230 250 6 (POTENTIAL).
FT DOMAIN 251 260 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 261 281 7 (POTENTIAL).
FT DOMAIN 282 297 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 163 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 297 AA; 34202 MW; EC2C1EA806571F80 CRC64;

Query Match 7.4%; Score 89; DB 1; Length 297;
Best Local Similarity 24.7%; Pred. No. 0.96;
Matches 48; Conservative 30; Mismatches 76; Indels 40; Gaps 9;

Qy 21 VRTGTYLLGVWYLLINAVLLILLISA-----LADPPQYNFSSSELGGDFEFDANWC 74
Db 9 VFAASVFLNFGVIANLFIIVIIKTNWSRRIASPRILFS-----L 51
```


FT TRANSMEM 1126 1146 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 1147 1203 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1204 1222 S1 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1223 1237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1238 1257 S2 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1258 1264 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1265 1286 S3 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1287 1311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1312 1331 S4 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1332 1350 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1351 1370 S5 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1371 1437 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1438 1462 S6 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1463 1610 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1 6 POLY-MET.
FT DOMAIN 652 658 POLY-LEU.
FT DOMAIN 826 836 POLY-GLU.
FT DOMAIN 428 445 BINDING TO THE BETA SUBUNIT
(BY SIMILARITY).
FT SITE 363 363 CALCIUM ION SELECTIVITY AND PERMEABILITY
(BY SIMILARITY).
FT SITE 704 704 CALCIUM ION SELECTIVITY AND PERMEABILITY
(BY SIMILARITY).
FT SITE 1099 1099 CALCIUM ION SELECTIVITY AND PERMEABILITY
(BY SIMILARITY).
FT SITE 1404 1404 CALCIUM ION SELECTIVITY AND PERMEABILITY
(BY SIMILARITY).
FT BINDING 1073 1163 DIHYDROPYRIDINES (BY SIMILARITY).
FT BINDING 1418 1484 DIHYDROPYRIDINES (BY SIMILARITY).
FT BINDING 1430 1473 PHENYLALKYLAMINES (BY SIMILARITY).
FT MOD RES 1473 1473 PHOSPHORYLATION (BY PKA) (POTENTIAL).
FT CA BIND 1491 1502 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 328 328 GFSDAMTFDSLVIGSIIDVASEADPTESLPTAT
FT VARSPLIC 1261 1303 PG -> HYFTDAMTFDALIVGVSDVIAIEVN (in
isoform CACH3D).
FT FT /FTId=VSP 000915.
SQ SEQUENCE 1610 AA; 182327 MW; B3B2E3794D936F79 CRC64;
Query Match 7.4%; Score 88.5; DB 1; Length 1610;
Best Local Similarity 25.0%; Pred. No. 5.7;
Matches 46; Conservative 34; Mismatches 61; Indels 43; Gaps 10;
Qy 21 VRTGILLGVYLLINAVLLILSALA----DP-DQVNSSSELG-GDPEFMDANMCI 74
Db 873 IRVGHKLNHIFTNLILVFMLSAALAEEDPIRSHSPFNTILGYFDYAF----- 924
Qy 75 AIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFQFALNMLVAITVLIYPNSIQBYIR 134
Db 925 -TAIFTVEILL-KMTTFGAPLHKG-----FCRYFNIL-LDMLVGVSLV----- 966
Qy 135 QLPNFPYRDVMSVNPCLVLIILLFISILITPKG--YLISCWNCVRYINGNSSDVL 192
Db 967 ----SFGIQSSAISVVKILRLVRLPLRAINRAKGLKHVVQCQVFAIRTI-----GNIM 1017
Qy 193 VYVT 196
Db 1018 IVTT 1021
RESULT 12
CCAD HUMAN
ID CCAD HUMAN STANDARD; PRT; 2161 AA.
AC Q01668; Q13916; Q13931;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Voltage-dependent L-type calcium channel alpha-1D subunit (Calcium
channel, L type, alpha-1 polypeptide, isoform 2).
GN CACNL1A2 OR CACNL1A2 OR CCHL1A2 OR CACH3 OR CACH4.
OS Homo sapiens (Human).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM NEURONAL-TYPE).
RC TISSUE=Neuroblastoma;
RX MEDLINE=92110010; PubMed=1309651;
RA Williams M.E., Feldman D.H., McCue A.F., Brenner R., Velicelebi G.,
RA Ellis S.B., Harpold M.M.;
RT "Structure and functional expression of alpha 1, alpha 2, and beta
subunits of a novel human neuronal calcium channel subtype.";
RL Neuron 8:71-84(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA-CELL-TYPE).
RC TISSUE=Pancreatic islets;
RX MEDLINE=92115705; PubMed=1309948;
RA Seino S., Chen L., Seino M., Blondel O., Takeda J., Johnson J.H.,
RA Bell G.I.;
RT "Cloning of the alpha 1 subunit of a voltage-dependent calcium
channel expressed in pancreatic beta cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:584-588(1992).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM BETA-CELL-TYPE), AND VARIANT NIDDM.
RX MEDLINE=96044438; PubMed=7557998;
RA Yamada Y., Masuda K., Li Q., Ihara Y., Kubota A., Miura T.,
RA Nakamura K., Fujii Y., Seino S., Seino Y.;
RT "The structures of the human calcium channel alpha 1 subunit
(CACNL1A2) and beta subunit (CACNLB3) genes.";
RL Genomics 27:312-319(1995).
CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1D
GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE)
CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)
GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP),
PHENYLALKYLAMINES, BENZOTHAZEPINES, AND BY OMEGA-ACETOXIN-IIIA
(OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-
GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=Neuronal-type;
IsoId=Q01668-1; Sequence=Displayed;
Name=Beta-cell-type;
IsoId=Q01668-2; Sequence=VSP_000914; VSP 000914;
CC -1- TISSUE SPECIFICITY: EXPRESSED IN PANCREATIC ISLETS AND IN BRAIN,
WHERE IT HAS BEEN SEEN IN HIPPOCAMPUS, BASAL GANGLIA, HABENULA AND
THALAMUS. NO EXPRESSION IN SKELETAL MUSCLE.
CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC -1- POLYMORPHISM: A CHANGE FROM SEVEN TO EIGHT ATG TRINUCLEOTIDE
REPEATS, RESULTING IN AN ADDITIONAL N-TERMINAL METHIONINE, HAS
BEEN FOUND IN A PATIENT WITH NON-INSULIN-DEPENDENT DIABETES
MELLITUS (NIDDM).
CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; M76558; AAA58402.1; -
 CC EMBL; M83566; AAA35629.1; -
 CC EMBL; D43747; BAA07804.1; -
 CC EMBL; D43705; BAA07804.1; JOINED.
 CC EMBL; D43706; BAA07804.1; JOINED.
 CC EMBL; D43707; BAA07804.1; JOINED.
 CC EMBL; D43708; BAA07804.1; JOINED.
 CC EMBL; D43709; BAA07804.1; JOINED.
 CC EMBL; D43710; BAA07804.1; JOINED.
 CC EMBL; D43711; BAA07804.1; JOINED.
 CC EMBL; D43712; BAA07804.1; JOINED.
 CC EMBL; D43713; BAA07804.1; JOINED.
 CC EMBL; D43714; BAA07804.1; JOINED.
 CC EMBL; D43715; BAA07804.1; JOINED.
 CC EMBL; D43716; BAA07804.1; JOINED.
 CC EMBL; D43717; BAA07804.1; JOINED.
 CC EMBL; D43718; BAA07804.1; JOINED.
 CC EMBL; D43719; BAA07804.1; JOINED.
 CC EMBL; D43720; BAA07804.1; JOINED.
 CC EMBL; D43721; BAA07804.1; JOINED.
 CC EMBL; D43722; BAA07804.1; JOINED.
 CC EMBL; D43723; BAA07804.1; JOINED.
 CC EMBL; D43724; BAA07804.1; JOINED.
 CC EMBL; D43725; BAA07804.1; JOINED.
 CC EMBL; D43726; BAA07804.1; JOINED.
 CC EMBL; D43727; BAA07804.1; JOINED.
 CC EMBL; D43728; BAA07804.1; JOINED.
 CC EMBL; D43729; BAA07804.1; JOINED.
 CC EMBL; D43730; BAA07804.1; JOINED.
 CC EMBL; D43731; BAA07804.1; JOINED.
 CC EMBL; D43732; BAA07804.1; JOINED.
 CC EMBL; D43733; BAA07804.1; JOINED.
 CC EMBL; D43734; BAA07804.1; JOINED.
 CC EMBL; D43735; BAA07804.1; JOINED.
 CC EMBL; D43736; BAA07804.1; JOINED.
 CC EMBL; D43737; BAA07804.1; JOINED.
 CC EMBL; D43738; BAA07804.1; JOINED.
 CC EMBL; D43739; BAA07804.1; JOINED.
 CC EMBL; D43740; BAA07804.1; JOINED.
 CC EMBL; D43741; BAA07804.1; JOINED.
 CC EMBL; D43742; BAA07804.1; JOINED.
 CC EMBL; D43743; BAA07804.1; JOINED.
 CC EMBL; D43744; BAA07804.1; JOINED.
 CC EMBL; D43745; BAA07804.1; JOINED.
 CC EMBL; D43746; BAA07804.1; JOINED.
 CC EMBL; HGNC:1391; CACNAID.
 CC MIM; 114206; -
 CC GO; GO:0005891; C: voltage-gated calcium channel complex; TAS.
 CC GO; GO:0015270; F: dihydropyridine-sensitive calcium channel a.; TAS.
 CC GO; GO:0006832; P: small molecule transport; TAS.
 CC InterPro; IPR001682; Ca/Na pore.
 CC InterPro; IPR002077; Ca channel.
 CC InterPro; IPR002111; Ca channel_TrpL.
 CC InterPro; IPR005821; Ion trans.
 CC InterPro; IPR005446; LVDCALphal.
 CC InterPro; IPR005452; LVDCALphalD.
 CC InterPro; IPR005920; M+channel_nlg.
 CC Pfam; PF00520; Ion trans. 4.
 CC PRINTS; PR00167; CACHANNEL.
 CC PRINTS; PR01630; LVDCALPHAL.
 CC PRINTS; PR01636; LVDCALPHALD.
 CC Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Calcium channel; Glycoprotein; Repeat; Multigene family;
 CC Calcium-binding; Phosphorylation; Alternative splicing; Polymorphism;
 CC Triplet repeat expansion.
 FT REPEAT 113 409 I.
 FT REPEAT 509 755 II.
 FT REPEAT 873 1155 III.

FT REPEAT 1192 1467 IV.
 FT DOMAIN 1 126 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 127 145 S1 OF REPEAT I (POTENTIAL).
 FT DOMAIN 146 163 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 164 183 S2 OF REPEAT I (POTENTIAL).
 FT DOMAIN 184 195 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 196 214 S3 OF REPEAT I (POTENTIAL).
 FT DOMAIN 215 235 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 236 254 S4 OF REPEAT I (POTENTIAL).
 FT DOMAIN 255 273 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 274 293 S5 OF REPEAT I (POTENTIAL).
 FT DOMAIN 294 381 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 382 406 S6 OF REPEAT I (POTENTIAL).
 FT DOMAIN 407 523 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 524 543 S1 OF REPEAT II (POTENTIAL).
 FT DOMAIN 544 558 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 559 577 S2 OF REPEAT II (POTENTIAL).
 FT DOMAIN 578 585 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 586 604 S3 OF REPEAT II (POTENTIAL).
 FT DOMAIN 605 614 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 615 633 S4 OF REPEAT II (POTENTIAL).
 FT DOMAIN 634 652 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 653 673 S5 OF REPEAT II (POTENTIAL).
 FT DOMAIN 674 727 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 728 752 S6 OF REPEAT II (POTENTIAL).
 FT DOMAIN 753 886 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 887 905 S1 OF REPEAT III (POTENTIAL).
 FT DOMAIN 906 921 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 922 941 S2 OF REPEAT III (POTENTIAL).
 FT DOMAIN 942 953 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 954 972 S3 OF REPEAT III (POTENTIAL).
 FT DOMAIN 973 978 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 979 998 S4 OF REPEAT III (POTENTIAL).
 FT DOMAIN 999 1017 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1018 1037 S5 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1038 1127 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1128 1148 S6 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1149 1205 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1206 1224 S1 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1225 1239 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1240 1259 S2 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1260 1266 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1267 1288 S3 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1289 1313 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1314 1333 S4 OF REPEAT IV (POTENTIAL).
 Query Match 7.4%; Score 88.5; DB 1; Length 2161;
 Best Local Similarity 25.0%; Pred. No. 7.6;
 Matches 46; Conservative 34; Mismatches 61; Indels 43; Gaps 10;
 Qy 21 VRTGILLGVYLLINAVLLILLALSA---DP-DQYFNSSSELG-GDREFMDANNCI 74
 Db 875 IRVCHKLINHIPTNLILFIMUSSAALAEEDPIRSHSFNTILGFVDFYAF----- 926
 Qy 75 AIAISLMILICAMATYGAQKQAAWIIPFFCYQIFDFALMLVAITVLIYPSIQEYIR 134
 Db 927 -TAFTVEILL-KMTTFGFLHKA----FCRNVENL-LDMLVGVSLV----- 968
 Qy 135 QLPNFPYRDDVMSNPTCLVLIILFISILITPKG--YLISCVWNCVRYINGRNSDVL 192
 Db 969 ----SFGIQSSAISVWKILRVLRPLRAINRAKGLKHVVQCVFAIRTI-----GNIM 1019
 Qy 193 VYVT 196
 Db 1020 IVTT 1023
 RESULT 13
 CCAD RAT
 ID CCAD RAT STANDARD; PRT: 2203 AA.
 AC P27732; O09022; O09023; Q01542; Q62691; Q62815; Q63491;
 AC Q63492;
 DT 01-OCT-1996 (Rel. 34, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Voltage-dependent L-type calcium channel alpha-1D subunit (Calcium
DE channel, L type, alpha-1 polypeptide, isoform 2) (Rat brain class D)
DE (RBD)
GN CACNA1D OR CACNA1L2 OR CCHL1A2 OR CACH3 OR CACNA4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Inullinoma;
RX MEDLINE=95280950; PubMed=7760845;
RA Ihara Y., Yamada Y., Fujii Y., Gono T., Yano H., Yasuda K.,
RA Inagaki N., Seino Y., Seino S.;
RT "Molecular diversity and functional characterization of voltage-
RT dependent calcium channels (CACNA4) expressed in pancreatic beta-
RT cells.";
RL Mol. Endocrinol. 9:121-130(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 3; 6; 7; 8 AND 14).
RC TISSUE=Brain;
RX MEDLINE=91293338; PubMed=1648940;
RA Hui A., Ellinor P.T., Krikanova O., Wang J.-J., Diebold R.J.,
RA Schwartz A.;
RT "Molecular cloning of multiple subtypes of a novel rat brain isoform
RT of the alpha-1 subunit of the voltage-dependent calcium channel.";
RL Neuron 7:35-44(1991).
RN [3]
RP SEQUENCE OF 1-125 FROM N.A.
RX MEDLINE=96040125; PubMed=7553731;
RA Kamp T.J., Mitas M., Fields K.L., Asch S., Chin H., Marban E.,
RA Nirenberg M.;
RT "Transcriptional regulation of the neuronal L-type calcium channel
RT alpha 1D subunit gene.";
RL Cell. Mol. Neurobiol. 15:307-326(1995).
RN [4]
RP SEQUENCE OF 1100-1410 FROM N.A. (ISOFORMS 11 AND 12).
RC TISSUE=Kidney;
RX MEDLINE=93066265; PubMed=1279681;
RA Yu A.S.L., Hebert S.C., Brenner B.M., Lytton J.;
RT "Molecular characterization and nephron distribution of a family of
RT transcripts encoding the pore-forming subunit of Ca2+ channels in the
RT kidney.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10494-10498(1992).
RN [5]
RP SEQUENCE OF 1200-1493 FROM N.A. (ISOFORMS 3; 4; 5; 9 AND 10).
RC TISSUE=Hepatoma;
RX MEDLINE=96074617; PubMed=7479909;
RA Barry E.L.R., Gesek F.A., Froehner S.C., Friedman P.A.;
RT "Multiple calcium channel transcripts in rat osteosarcoma cells:
RT selective activation of alpha 1D isoform by parathyroid hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:10914-10918(1995).
RN [6]
RP SEQUENCE OF 1200-1493 FROM N.A. (ISOFORMS 3; 4; 5; 9 AND 10).
RC TISSUE=Hepatoma;
RX MEDLINE=97376179; PubMed=9232351;
RA Brereton H.M., Harland M.L., Frosio M., Petronijevic T.,
RA Barrett G.J.;
RT "Novel variants of voltage-operated calcium channel alpha-1 subunit
RT transcripts in a rat liver-derived cell line: deletion in the IVS4
RT voltage sensing region.";
RL Cell Calcium 22:39-52(1997).
RN [7]
RP SEQUENCE OF 1307-1479 FROM N.A. (ISOFORM 3).
RX MEDLINE=90239020; PubMed=1692134;
RA Snutch T.P., Leonard J.P., Gilbert M.M., Lester H.A., Davidson N.;
RT "Rat brain expresses a heterogeneous family of calcium channels.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3391-3395(1990).
CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE

CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1D
CC GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE)
CC CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)
CC GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP), AGATOXIN-11A
CC PHENYALKYLAMINES, BENZOTHAZEPINES, AND BY OMEGA-AGATOXIN-11A
CC (OMEGA-AGA-11A). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-
CC GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=14;
CC Comment=The region sequenced in isoforms ROB3 and RKC5 is
CC identical to CACNA4;
CC Name=1; Synonyms=CACNA4A;
CC IsoId=P27732-1; Sequence=Displayed;
CC Name=2; Synonyms=CACNA4B;
CC IsoId=P27732-2; Sequence=VSP_000923, VSP_000924;
CC Name=3; Synonyms=CACH3A, RB48, RBD-55;
CC IsoId=P27732-3; Sequence=VSP_000921;
CC Name=4; Synonyms=Delta-IV-S3;
CC IsoId=P27732-4; Sequence=VSP_000919;
CC Name=5; Synonyms=Delta-IV-S4;
CC IsoId=P27732-5; Sequence=VSP_000922;
CC Name=6; Synonyms=RB9;
CC IsoId=P27732-6; Sequence=VSP_000920, VSP_000921;
CC Name=7; Synonyms=RB11;
CC IsoId=P27732-7; Sequence=VSP_000917;
CC Name=8; Synonyms=RB34;
CC IsoId=P27732-8; Sequence=VSP_000916;
CC Name=9; Synonyms=RH1;
CC IsoId=P27732-9; Sequence=VSP_000918;
CC Name=10; Synonyms=RH2;
CC IsoId=P27732-10; Sequence=VSP_000919, VSP_000922;
CC Name=11; Synonyms=RKC5;
CC IsoId=P27732-13; Sequence=Not described;
CC Name=12; Synonyms=RKC6;
CC IsoId=P27732-11; Sequence=VSP_000919;
CC Name=13; Synonyms=ROB3;
CC IsoId=P27732-14; Sequence=Not described;
CC Name=14; Synonyms=Truncated;
CC IsoId=P27732-12; Sequence=VSP_000925, VSP_000926;
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, PANCREATIC ISLETS AND B-
CC LYMPHOCYTES.
CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
CC FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)
CC or send an email to license@isb-sib.ch.
CC -----
CC EMBL; D38101; BAA07282.1; -
CC EMBL; D38102; BAA07283.1; -
CC EMBL; M57682; AAA42015.1; -
CC EMBL; U14005; AAB60515.1; -
CC EMBL; M92221; AAA40895.1; -
CC EMBL; U31772; AAA89156.1; -
CC EMBL; U49126; AAB61634.1; -

DR EMBL; U49127; AAB61635.1; --
DR EMBL; U49128; AAB61636.1; --
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002077; Ca_channel.
DR InterPro; IPR002111; Ca_channel_TrpL.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR005446; LVDCCAlphal.
DR InterPro; IPR005452; LVDCCAlphald.
DR InterPro; IPR005820; Mchannel_nlg.
DR Pfam; PF00520; Ion_chan; 4.
DR PRINTS; PRO0167; CACHANNEL.
DR PRINTS; PRO0169; KCHANNEL.
DR PRINTS; PRO1630; LVDCCAlphal.
DR PRINTS; PRO1636; LVDCCAlphald.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Calcium channel; Glycoprotein; Repeat; Multigene family;
KW Calcium-binding; Phosphorylation; Alternate splicing.
FT REPEAT 112 408 I.
FT REPEAT 528 774 II.
FT REPEAT 892 1174 III.
FT REPEAT 1211 1486 IV.
FT DOMAIN 1 126 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 127 145 S1 OF REPEAT I (POTENTIAL).
FT DOMAIN 146 163 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 164 183 S2 OF REPEAT I (POTENTIAL).
FT DOMAIN 184 195 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 196 214 S3 OF REPEAT I (POTENTIAL).
FT DOMAIN 215 235 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 236 254 S4 OF REPEAT I (POTENTIAL).
FT DOMAIN 255 273 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 274 293 S5 OF REPEAT I (POTENTIAL).
FT DOMAIN 294 381 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 382 406 S6 OF REPEAT I (POTENTIAL).
FT DOMAIN 407 582 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 583 602 S1 OF REPEAT II (POTENTIAL).
FT DOMAIN 603 617 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 618 636 S2 OF REPEAT II (POTENTIAL).
FT DOMAIN 637 644 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 645 663 S3 OF REPEAT II (POTENTIAL).
FT DOMAIN 664 673 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 674 692 S4 OF REPEAT II (POTENTIAL).
FT DOMAIN 693 711 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 712 732 S5 OF REPEAT II (POTENTIAL).
FT DOMAIN 733 786 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 787 811 S6 OF REPEAT II (POTENTIAL).
FT DOMAIN 812 945 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 946 964 S1 OF REPEAT III (POTENTIAL).
FT DOMAIN 965 980 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 981 1000 S2 OF REPEAT III (POTENTIAL).

Query Match 7.4%; Score 88.5; DB 1; Length 2203;
Best Local Similarity 25.0%; Pred. No. 7.8;
Matches 46; Conservative 34; Mismatches 61; Indels 43; Gaps 10;

Qy 21 VRTGTLGVWYLIINAVLLILLSALA-----DP-DVNFSSSELG-GDFFEMDDANNCI 74
Db IRVGCCKLNIHFNLIVFIMLSAALAEEDPIRSHSFNTILGYFDYAF----- 985

Qy 75 AIALSLMLICAMATYGAKQRAAWIIPFCYQIFDFALNMLVAITVLIYPSIQEYR 134
Db -TAFTVEILL-KWTFCAFLHKA-----FCRNYFNL-LDMLVVGSLV----- 1027

Qy 135 QLPNPPFPDDVMSVNPCLVLIILFISILITFKG--YLISCWNCVRYINGRSSDVL 192
Db ----SFGIQSSAISVVKILRVLRPLRINRAKGLKHVVQCVPVAIRTI-----GNIM 1078

Qy 193 VVVT 196
Db 1079 IVTT 1082

RESULT 14

NU2M DROMA
ID NU2M DROMA STANDARD; PRT; 274 AA.
AC P2987;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3) (Fragment).
GN ND2.
OS Drosophila mauritiana (Fruit fly).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7226;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91088557; PubMed=2124697;
RX Satta Y., Takahata N.;
RT "Evolution of Drosophila mitochondrial DNA and the history of the
RT melanogaster subgroup."
RL Proc. Natl. Acad. Sci. U.S.A. 87:9558-9562(1990).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M57912; AAA99050.1; --
DR FlyBase; FBgn0012512; Dmau\mt:ND2.
DR InterPro; IPR003917; NADHub_oxred2.
DR InterPro; IPR003916; NADHub_oxred5.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
DR PRINTS; PRO1436; NADHDHGNASE2.
DR PRINTS; PRO1434; NADHDHGNASES.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
FT NON TER 1
SQ SEQUENCE 274 AA; 32226 MW; BB27336F8E8ED40B CRC64;

Query Match 7.3%; Score 88; DB 1; Length 274;
Best Local Similarity 21.0%; Pred. No. 1.1;
Matches 37; Conservative 29; Mismatches 56; Indels 54; Gaps 6;

Qy 28 LGVWYLIINAVLLILLSALADPDQYN-----FSS-SELGGDFEPMDDANMCIAISL 80
Db LNIKYLILSVLSVIGLGAIGGLNQTSLRKMAFSSINHLGW-----MLSS 122

Qy 81 LMLICAMATYGAKQRAAWIIPFCYQIFDFALNMLVAITVLIYPSIQEYR----- 132
Db LMI-----SSSIWLIYFFFSFLSVLTFMFNIFKLPHLQLPFSWFSVKILK 170

Qy 133 -----TRQPPNPPFPDDVMSVNPCL-----VLIILFISILITFKGYLISC 175
Db FTLPNMFSLGGLPPFLGFLPKWLVIOQLTLCNOYFLLMLLMSTLITLFFYLKIC 226

RESULT 15
MTR_NEUCR
ID MTR_NEUCR STANDARD; PRT; 470 AA.
AC P38680;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE N amino acid transport system protein (Methyltryptophan resistance
DE protein).
GN MTR.

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2004, 14:19:40 ; Search time 35 Seconds
(without alignments)
1666.283 Million cell updates/sec

Title: US-09-965-529-26
Perfect score: 1200
Sequence: 1 MKMVAPWTRFYSNCSCLCCH.....YDDATVNGAAKEPPPPYVSA 226

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_page.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1200	100.0	226	4 Q9H060	Q9H060 homo sapien
2	1200	100.0	283	4 Q9NY06	Q9NY06 homo sapien
3	1113.5	92.8	227	11 Q91X06	Q91X06 mus musculu
4	552.5	46.0	233	11 Q8BG66	Q8BG66 mus musculu
5	550.5	45.9	233	4 Q9BTU8	Q9BTU8 homo sapien
6	432.5	36.0	197	11 Q9CRX2	Q9CRX2 mus musculu
7	315	26.2	313	5 Q964G6	Q964G6 bombyx mori
8	287.5	24.0	421	5 Q9MKR3	Q9MKR3 drosophila
9	287.5	24.0	428	5 Q9SR82	Q9SR82 drosophila
10	282.5	23.5	432	5 Q9V4X3	Q9V4X3 drosophila
11	170	14.2	261	11 Q9JJ55	Q9JJ55 rattus norv
12	157	13.1	286	5 Q9BLM6	Q9BLM6 schistosoma
13	156	13.0	261	11 Q9BFZ0	Q9BFZ0 mus musculu
14	146.5	12.2	281	5 Q9U597	Q9U597 schistosoma
15	122	10.2	165	5 Q9VEW3	Q9VEW3 drosophila
16	115	9.6	236	5 Q23190	Q23190 caenorhabdi

17	102.5	8.5	235	5	Q17664	Q17664 caenorhabdi
18	101.5	8.5	419	5	Q95Q81	Q95Q81 caenorhabdi
19	99.5	8.3	315	16	Q92T11	Q92T11 rhizobium m
20	99.5	8.3	672	3	Q04562	Q04562 saccharomyc
21	99	8.2	263	2	Q05370	Q05370 actinobacil
22	98.5	8.2	156	12	Q9EMQ1	Q9EMQ1 amsacta moo
23	97.5	8.1	627	5	Q81J19	Q81J19 plasmodium
24	96	8.0	151	5	Q17650	Q17650 caenorhabdi
25	95.5	8.0	282	11	Q9JJ42	Q9JJ42 rattus norv
26	94.5	7.9	240	5	Q18527	Q18527 caenorhabdi
27	94	7.8	250	5	Q9VZL8	Q9VZL8 drosophila
28	94	7.8	260	16	Q8E5Q4	Q8E5Q4 streptococ
29	93.5	7.8	221	5	Q45310	Q45310 caenorhabdi
30	93.5	7.8	301	5	Q19757	Q19757 caenorhabdi
31	93	7.8	1351	11	Q02789	Q02789 mus musculu
32	91.5	7.6	185	10	Q9M878	Q9M878 arabidopsis
33	91.5	7.6	1032	16	Q9A7D5	Q9A7D5 caulobacter
34	91	7.6	343	8	Q9Z238	Q9Z238 trichophyto
35	91	7.6	3535	5	Q8IC29	Q8IC29 plasmodium
36	90	7.5	161	8	Q9XN18	Q9XN18 euglena gra
37	90	7.5	540	5	Q8IC17	Q8IC17 plasmodium
38	89.5	7.5	237	5	Q20508	Q20508 caenorhabdi
39	89.5	7.5	293	8	Q8HET6	Q8HET6 formica tru
40	89.5	7.5	341	8	Q9MGL3	Q9MGL3 drosophila
41	89	7.4	241	5	Q9VLI3	Q9VLI3 drosophila
42	89	7.4	297	11	Q9JKT3	Q9JKT3 mus musculu
43	89	7.4	382	2	Q8KN98	Q8KN98 pseudomonas
44	89	7.4	391	16	Q92721	Q92721 listeria in
45	89	7.4	1543	4	Q8WWZ4	Q8WWZ4 homo sapien

ALIGNMENTS

RESULT 1

Q9H060	PRELIMINARY;	PRT;	226 AA.
ID	Q9H060		
AC	Q9H060;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)		
DE	Hypothetical protein NP2RM1000066 (Putative integral membrane protein)		
DE	(lysosomal-associated transmembrane protein 4 beta) (Putative integral		
DE	membrane transporter).		
GN	DKFZP586B1124 OR LAPT4BETA.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Uterus;		
RA	MEDLINE=21154917; PubMed=11230166;		
RA	Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,		
RA	Ansorge W., Boecker M., Bloeker H., Bauersachs S., Blum H.,		
RA	Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,		
RA	Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,		
RA	Wambutt R., Korn B., Klein M., Routska A.;		
RT	"Towards a Catalog of Human Genes and Proteins: Sequencing and		
RT	Analysis of 500 Novel Complete Protein Coding Human cDNAs.";		
RL	Genome Res. 11:422-435(2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Shao G., Zhou R.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Eye;		
RA	Strausberg R.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RA	Hogue D.L.;		

RT "Identification of a novel LAPTM cDNA."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strauberg R.;

RN Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.

RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isegai T.;

RN "HRI human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL136942; CAB66876.1; -
DR EMBL; AY057051; AAL17908.1; -
DR EMBL; BC014129; AAH14129.1; -
DR EMBL; AF317417; AAK69595.1; -
DR EMBL; BC031021; AAH31021.1; -
DR EMBL; AK075326; BAC11549.1; -
DR InterPro; IPR004687; Mtp.

DR Pfam; PF03821; Mtp; 1.
KW Hypothetical protein; Transmembrane.
SQ SEQUENCE 226 AA; 25419 MW; A3156D2F2C0DCF0B CRC64;

Query Match 100.0%; Score 1200; DB 4; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.4e-108;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYNSCCLCHVTRGTILLGWYLIINAVLLILLSALADPDQYFSSSEL 60
Db 1 MKWVAPWTRFYNSCCLCHVTRGTILLGWYLIINAVLLILLSALADPDQYFSSSEL 60

Qy 61 GGDFFMDANMCIAISLMLICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDFFMDANMCIAISLMLICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120

Qy 121 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLILLFISILTFKGYLISCVWNCY 180
Db 121 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLILLFISILTFKGYLISCVWNCY 180

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 2
Q9NY06 PRELIMINARY; PRT; 283 AA.

DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Integral membrane transporter protein.
GN LC27.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OK NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Liu J., Zhang J., Zhou R., Jin C.;

RT "Molecular cloning and preliminary study on biological function of a
RT novel gene overexpressed in human hepatocellular carcinoma."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ276485; CAB81951.1; -
DR EMBL; HGNC:13646; LAPTM4B.
DR InterPro; IPR004687; Mtp.
DR Pfam; PF03821; Mtp; 1.

SQ SEQUENCE 283 AA; 31735 MW; B384B42CD83B2B11 CRC64;
Query Match 100.0%; Score 1200; DB 4; Length 283;

Best Local Similarity 100.0%; Pred. No. 1.8e-108;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYNSCCLCHVTRGTILLGWYLIINAVLLILLSALADPDQYFSSSEL 60
Db 58 MKWVAPWTRFYNSCCLCHVTRGTILLGWYLIINAVLLILLSALADPDQYFSSSEL 117

Qy 61 GGDFFMDANMCIAISLMLICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 118 GGDFFMDANMCIAISLMLICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 177

Qy 121 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLILLFISILTFKGYLISCVWNCY 180
Db 178 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLILLFISILTFKGYLISCVWNCY 237

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

RESULT 3
Q91XQ6 PRELIMINARY; PRT; 227 AA.

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Lysosomal-associated transmembrane protein 4 beta
DE (Lysosomal-associated protein transmembrane 4B).
GN LAPTM4B.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OK NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RA Hogue D.L.;

RC STRAIN=C57BL; TISSUE=Brain;
RT "Identification of a novel LAPTM cDNA."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Strauberg R.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Hypothalamus, Ovary, Testis, and Uterus;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium.

RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AF317418; AAK69596.1; -
DR EMBL; BC019120; AAH19120.1; -
DR EMBL; AK077269; BAC36721.1; -
DR EMBL; AK077933; BAC37072.1; -
DR EMBL; AK079581; BAC37691.1; -
DR EMBL; AK082807; BAC38630.1; -
DR MGD; MGI:1890494; Laptm4b.
DR InterPro; IPR004687; Mtp.
DR Pfam; PF03821; Mtp; 1.

KW Transmembrane.
SQ SEQUENCE 227 AA; 25395 MW; FD3DC53C2682818D CRC64;

Query Match 92.8%; Score 1113.5; DB 11; Length 227;
Best Local Similarity 92.1%; Pred. No. 3.6e-100;
Matches 209; Conservative 9; Mismatches 8; Indels 1; Gaps 1;

Qy 1 MKWVAPWTRFYNSCCLCHVTRGTILLGWYLIINAVLLILLSALADPDQYFSSSEL 60
Db 1 MKWVAPWTRFYNSCCLCHVTRGTILLGWYLIINAVLLILLSALADPDQYFSSSEL 60

```
QY 61 GGDFFEMDDANMCIAISLLMILICAMATYGAYKQRAAWIIPFFCYOIFDPALNMLVAI 120
DB 61 GGEFFEMDDANMCIAISLLMILICAMATYGAYKQRAAWIIPFFCYOIFDPALNMLVAI 120
QY 121 TVLIYVNSIQEYIROLPNPFPYRDDVMSVNPCTCLVLIILLFISIIITLTKGYLISCVW 180
DB 121 TVLVYVNSIQEYIROLPNPFPYRDDVMSVNPCTCLVLIILLFISIIITLTKGYLISCVW 180
QY 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDAT-VNGAAKEPPPPYVSA 226
DB 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDATVPSTAKEPPPPYVSA 227

RESULT 4
Q8BTU8 PRELIMINARY; PRT; 233 AA.
AC Q8BG66;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Lysosomal-associated protein transmembrane 4A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body, Heart, and Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.",
RL Nature 420:563-573 (2002).
DR EMBL; AK075699; BAC35897.1; -
DR EMBL; AK084515; BAC39207.1; -
DR EMBL; AK088958; BAC40672.1; -
SQ SEQUENCE 233 AA; 26813 MW; BP60C9722A9DFDBD CRC64;

Query Match 46.0%; Score 552.5; DB 11; Length 233;
Best Local Similarity 45.2%; Pred. No. 1e-45;
Matches 104; Conservative 44; Mismatches 61; Indels 21; Gaps 6;

QY 9 RPYNSCCLCCHVRTGTTILGWVYLIINAVLLIILSLALDPD-----QY----NFSS 57
DB 13 RPYSTRCCGCHVRTGTTILGWVYVNVNLLMAILLTVETHPNSMPAVNIQYEVIGNYIS 72
QY 58 SELGGDFEFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFFCYOIFDPALNML 117
DB 73 SERMAD-----NACVLFAVSLVLMFISSMLVYGAISVQVGLIPFFCYRLDFVLSC 125
QY 118 VAITVLIYVNSIQEYIROLPNPFPYRDDVMSVNPCTCLVLIILLFISIIITLTKGYLISCVW 177
DB 126 VAISLTYLPRKEYLDQL-PDFPYKDLLALDSSCLLFIVLFFVFWFIIFKAYLINCW 184
QY 178 NCYRNGRNSDVLVY-VTSNDTTLVLLPPYDATVNGAAKEPPPPYVSA 226
DB 185 NCYKYINNRNVPETAVYFAFEPPOVLYPTVEMA-VKPIKEPPPPYLP 233

RESULT 5
Q8BTU8 PRELIMINARY; PRT; 233 AA.
AC Q8BTU8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Lysosomal-associated protein transmembrane 4 alpha.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

QY 61 GGDFFEMDDANMCIAISLLMILICAMATYGAYKQRAAWIIPFFCYOIFDPALNMLVAI 120
DB 61 GGEFFEMDDANMCIAISLLMILICAMATYGAYKQRAAWIIPFFCYOIFDPALNMLVAI 120
QY 121 TVLIYVNSIQEYIROLPNPFPYRDDVMSVNPCTCLVLIILLFISIIITLTKGYLISCVW 180
DB 121 TVLVYVNSIQEYIROLPNPFPYRDDVMSVNPCTCLVLIILLFISIIITLTKGYLISCVW 180
QY 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDAT-VNGAAKEPPPPYVSA 226
DB 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDATVPSTAKEPPPPYVSA 227

RESULT 4
Q8BTU8 PRELIMINARY; PRT; 233 AA.
AC Q8BG66;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Lysosomal-associated protein transmembrane 4A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body, Heart, and Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.",
RL Nature 420:563-573 (2002).
DR EMBL; AK075699; BAC35897.1; -
DR EMBL; AK084515; BAC39207.1; -
DR EMBL; AK088958; BAC40672.1; -
SQ SEQUENCE 233 AA; 26813 MW; BP60C9722A9DFDBD CRC64;

Query Match 46.0%; Score 552.5; DB 11; Length 233;
Best Local Similarity 45.2%; Pred. No. 1e-45;
Matches 104; Conservative 44; Mismatches 61; Indels 21; Gaps 6;

QY 9 RPYNSCCLCCHVRTGTTILGWVYLIINAVLLIILSLALDPD-----QY----NFSS 57
DB 13 RPYSTRCCGCHVRTGTTILGWVYVNVNLLMAILLTVETHPNSMPAVNIQYEVIGNYIS 72
QY 58 SELGGDFEFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFFCYOIFDPALNML 117
DB 73 SERMAD-----NACVLFAVSLVLMFISSMLVYGAISVQVGLIPFFCYRLDFVLSC 125
QY 118 VAITVLIYVNSIQEYIROLPNPFPYRDDVMSVNPCTCLVLIILLFISIIITLTKGYLISCVW 177
DB 126 VAISLTYLPRKEYLDQL-PDFPYKDLLALDSSCLLFIVLFFVFWFIIFKAYLINCW 184
QY 178 NCYRNGRNSDVLVY-VTSNDTTLVLLPPYDATVNGAAKEPPPPYVSA 226
DB 185 NCYKYINNRNVPETAVYFAFEPPOVLYPTVEMA-VKPIKEPPPPYLP 233

RESULT 5
Q8BTU8 PRELIMINARY; PRT; 233 AA.
AC Q8BTU8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Lysosomal-associated protein transmembrane 4 alpha.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```

```
QY 9 RPYNSCCLCCHVRTGTTILGWVYLIINAVLLIILSLALDPD-----QY----NFSS 57
DB 13 RPYSTRCCGCHVRTGTTILGWVYVNVNLLMAILLTVETHPNSMPAVNIQYEVIGNYIS 72
QY 58 SELGGDFEFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFFCYOIFDPALNML 117
DB 73 SERMAD-----NACVLFAVSLVLMFISSMLVYGAISVQVGLIPFFCYRLDFVLSC 125
QY 118 VAITVLIYVNSIQEYIROLPNPFPYRDDVMSVNPCTCLVLIILLFISIIITLTKGYLISCVW 177
DB 126 VAISLTYLPRKEYLDQL-PDFPYKDLLALDSSCLLFIVLFFVFWFIIFKAYLINCW 184
QY 178 NCYRNGRNSDVLVY-VTSNDTTLVLLPPYDATVNGAAKEPPPPYVSA 226
DB 185 NCYKYINNRNVPETAVYFAFEPPOVLYPTVEMA-VKPIKEPPPPYLP 233

RESULT 6
Q8CRX2 PRELIMINARY; PRT; 197 AA.
AC Q9CRX2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 13 days embryo head cDNA, RIKEN full-length enriched library,
DE clone:3110001N02 product:lysosomal-associated protein transmembrane
DE 4A, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Horii F.,
RA Imotani K., Ishii Y., Itoh M., Iwata M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RN Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.",
RL Nature 420:563-573 (2002).
RN [3]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=C57BL/6J; TISSUE=Head;
RA MEDLINE=21085660; PubMed=11217851;
RX RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX STRAIN=C57BL/6J; PubMed=10349636;
RX Carninci P., Hayashizaki Y.;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX STRAIN=C57BL/6J; PubMed=11042159;
RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX STRAIN=C57BL/6J; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Taehiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multipipette sequencer.";
RL Genome Res. 10:1757-1771(2000).
DR EMBL; AK013963; BAB29087.2; -
SQ SEQUENCE 197 AA; 22608 MW; 43CB906B0530761D CRC64;

Query Match 36.0%; Score 432.5; DB 11; Length 197;
Best Local Similarity 41.3%; Pred. No. 3.9e-34;
Matches 85; Conservative 43; Mismatches 57; Indels 21; Gaps 6;

QY 33 LIINAVLILLSALADPD-----QY-----NFSSSELGDFPFMDANNMCIAIAISLL 81
DB 1 MVNLLMAILTVEHTNSMPAVNIQEVIGNYSSEEMAD-----NACVLFAVSVL 53
QY 82 MILICAMATYGAAYKQRAAWIIPFCYQIFDPAALMLVAITVLIYNSIQEYIROLPPNFP 141
DB 54 MFIISMLVYGAISYQVGLIPFFCYRDFVLSCLVAISLTYLPRIKYLQDL-PDFP 112
QY 142 YRDVMSVNPCLVLIILFTSIIITKGYLISCVNVCYRYINGRSSDVLVY-VTSNDT 200
DB 113 YKDLLALDSSCLLFVLVFFVFIIFKAYLINCVMNVCYKYNINRNVPETAVYAFETPP 172
QY 201 TVLLPPYDDATVNGAAKEPPPPYVSA 226
DB 173 QYVLPTEYMA-VKPEKEPPPLPA 197

RESULT 7
Q964G6
ID Q964G6 PRELIMINARY; PRT; 313 AA.
AC Q964G6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Lysosomal-associated transmembrane protein.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
```

```
RP SEQUENCE FROM N.A.
RA Hogue D.L.;
RT "Identification of a LAPTM ortholog in Bombyx mori.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF317420; AAK69598.1; -
DR InterPro; IPR004687; Mtp.
DR Pfam; PF03821; Mtp; 1.
KW Transmembrane.
SQ SEQUENCE 313 AA; 34292 MW; 52CB6D97E0DB71C3 CRC64;

Query Match 26.2%; Score 315; DB 5; Length 313;
Best Local Similarity 29.0%; Pred. No. 1.6e-22;
Matches 76; Conservative 47; Mismatches 79; Indels 60; Gaps 8;

QY 15 CCLCCHVTCITILLGVWYLIINAVLILLSALADP---DOYNFSSSELG-----GD 63
DB 18 CCFLCHVTCITILLGVWYLIINAVLILLSALADP---DOYNFSSSELG-----GD 77
QY 64 F-----EFMDANNMCIAIAISLMLICAMATYGAAYKQRAAWIIPF 104
DB 78 VLPTLSNVETRPSYPQSASHSDHSLIYLGTMALTLMI-----YGAARGKPAVLLPF 132
QY 105 FCYQIFDPAALMLVAITVLIYNSIQEYIROLPPNFPYRDDVMSVNPCLVLIILFISI 164
DB 133 FCLQIFDFAITLTATGTCYLCRQIHAIHAE-TRRVPFBEELRLPAPALAFVVISALIV 191
QY 165 ILTFKGYLISCVNVCYRYINGRSS--DVLVYVTSNDTV-----LL 204
DB 192 AVIIGKVCISVWRVCYKYLTMRTAAQLSLTPFVVISDGI VTSAPAPPYPOPPDYSSLL 251
QY 205 PYDDATVNGAAKEPPPPYVSA 226
DB 252 PDYEAA-----VKQTPPSYEA 269

RESULT 8
Q8MKR3
ID Q8MKR3 PRELIMINARY; PRT; 421 AA.
AC Q8MKR3
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG14767-PA.
GN CG14767 OR C8575.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
```

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laiko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milehina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RN SEQUENCE FROM N.A.
 RA Celisner S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Hock J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirekas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celisner S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A.
 RA Adams M.D., Celisner S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB003836; AAM68833.1; -
 DR FlyBase; FBgn0040777; CG14767.
 DR InterPro; IPR004687; Mtp.
 DR Pfam; PF03821; Mtp; 1.
 SQ SEQUENCE 421 AA; 46079 MW; 84EE22F2F6F799AC CRC64;
 Query Match 24.0%; Score 287.5; DB 5; Length 421;
 Best Local Similarity 26.8%; Pred. No. 9.9e-20;
 Matches 71; Conservative 41; Mismatches 82; Indels 71; Gaps 7;
 Qy 14 SCCLCCHVRGCTILLGWYLLIINAVLLIL----- 43
 Db 32 TCCFGLHVHTATLMIGLWHLFLNLALSVLAVIWRNPEMDELEGTHDYTVLSAPALP 91
 Qy 44 --LSALADPDQY-----NFSSELGGDFEFMDANMCIA-IAISLLMLICAMATYGYK 95
 Db 92 TPLSKVEPPVAYRDSLSNYQNFDMGG-----LVCTCMIAITLMI-----YGTIK 136
 Qy 96 QRAAWIIPFCYQIFDFALNMLVAITVLPNSIQEYIRQLPPNPPYRDDVMSVNPCLV 155

Db 137 GKPSHLLPFFCLOLDFDAITTLTAAGYLCYLOAHSIIAE-SHRLPWREKLELPPBELV 195
 Qy 156 LIILLFISILITPKGYLISCVWNCYRYI-----NGRNSSDVLVYVTSN 198
 Db 196 VVVLVFIICVFLKAYCIGIIVWCYKYLTRQOHVRTLPPFLEPPTGVHSGVGTFGAER 255
 Qy 199 DTTVLLPPYDDATVNGAAKEPPPPY 223
 Db 256 SYSTLLPNYDEATAQYLKQAPPSPY 280
 RESULT 9
 Q95R82 PRELIMINARY; PRT; 428 AA.
 AC Q95R82;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE SD02746P.
 GN CG14767 OR CG8575.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celisner S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY61575; AAL29123.1; -
 DR FlyBase; FBgn0040777; CG14767.
 DR InterPro; IPR004687; Mtp.
 DR Pfam; PF03821; Mtp; 1.
 SQ SEQUENCE 428 AA; 47005 MW; 59F65579E88DB57D CRC64;
 Query Match 24.0%; Score 287.5; DB 5; Length 428;
 Best Local Similarity 26.8%; Pred. No. 1e-19;
 Matches 71; Conservative 41; Mismatches 82; Indels 71; Gaps 7;
 Qy 14 SCCLCCHVRGCTILLGWYLLIINAVLLIL----- 43
 Db 39 TCCFGLHVHTATLMIGLWHLFLNLALSVLAVIWRNPEMDELEGTHDYTVLSAPALP 98
 Qy 44 --LSALADPDQY-----NFSSELGGDFEFMDANMCIA-IAISLLMLICAMATYGYK 95
 Db 99 TPLSKVEPPVAYRDSLSNYQNFDMGG-----LVCTCMIAITLMI-----YGTIK 143
 Qy 96 QRAAWIIPFCYQIFDFALNMLVAITVLPNSIQEYIRQLPPNPPYRDDVMSVNPCLV 155
 Db 144 GKPSHLLPFFCLOLDFDAITTLTAAGYLCYLOAHSIIAE-SHRLPWREKLELPPBELV 202
 Qy 156 LIILLFISILITPKGYLISCVWNCYRYI-----NGRNSSDVLVYVTSN 198
 Db 203 VVVLVFIICVFLKAYCIGIIVWCYKYLTRQOHVRTLPPFLEPPTGVHSGVGTFGAER 262
 Qy 199 DTTVLLPPYDDATVNGAAKEPPPPY 223
 Db 263 SYSTLLPNYDEATAQYLKQAPPSPY 287
 RESULT 10
 Q9V4X3 PRELIMINARY; PRT; 432 AA.
 AC Q9V4X3; Q9V4X4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE CG14767 protein (Lysosomal-associated transmembrane protein).

```

GN CG14767 OR CG8575.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.J., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foaier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "the genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Hoque D.L.;
RT "Identification of a LAPTM ortholog in Drosophila melanogaster."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM ARE PRODUCED BY ALTERNATIVE SPLICING.
DR EMBL; AE003836; AAF59049.2; -
DR EMBL; AE003836; AAF59050.2; -
DR EMBL; AF317419; AAK69597.1; -
DR FlyBase; FBgn0040777; CG14767.
DR InterPro; IPR004687; Mtp.
DR Pfam; PF03821; Mtp; 1.
KW Alternative splicing; Transmembrane.
FT VARSPLIC 1 MISSING (IN SHORT ISOFORM).
SQ SEQUENCE 432 AA; 47609 MW; ADBB0CC036EC74C4 CRC64;

Query Match 23.5%; Score 282.5; DB 5; Length 432;
Best Local Similarity 26.4%; Pred. No. 3.1e-19;
Matches 68; Conservative 40; Mismatches 97; Indels 53; Gaps 5;

Qy 14 SCCLCHVCTGTTLLGWYLIINAVLLIISLALADPDQYNFSSSELGGDFEFMD-- 69
Db 39 TCCFGLVHTATMLIGLHVLNLTALSVLAVRNPEMD-----ELEGGHTDYDL 94

RESULT 12
Q9BLM6 PRELIMINARY; PRT; 286 AA.
ID Q9BLM6
AC Q9BLM6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)

Query Match 14.2%; Score 170; DB 11; Length 261;
Best Local Similarity 23.0%; Pred. No. 1.6e-08;
Matches 60; Conservative 47; Mismatches 90; Indels 64; Gaps 11;

Qy 14 SCCLCHVCTGTTLLGWYLIINAVLLIISLALADPDQYNFSSSELGGDFEFMD 71
Db 11 TCC-CFNVRVATVALAIYHIV-SVLLFIEHVVEVARGKVSRCFSK-----MPYLR 62

Query Match 14.2%; Score 170; DB 11; Length 261;
Best Local Similarity 23.0%; Pred. No. 1.6e-08;
Matches 60; Conservative 47; Mismatches 90; Indels 64; Gaps 11;

Qy 72 MCTAIAISLMLICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAITVLIYPSIQ 131
Db 63 LLSFLLIGLVLFISLSLFGVNNREKYLIPFLSLQIMDFLCLLLIGSYELPAYLK 122

Query Match 14.2%; Score 170; DB 11; Length 261;
Best Local Similarity 23.0%; Pred. No. 1.6e-08;
Matches 60; Conservative 47; Mismatches 90; Indels 64; Gaps 11;

Qy 132 YIRQLPFPFRRDDVMSVN--PTCLVLIILL----- 160
Db 123 FARPRG--PSKVPMLTLQLDFCLSLTLCSSVMEVPTVNFKNMNMVLPSEQCM 180

Query Match 14.2%; Score 170; DB 11; Length 261;
Best Local Similarity 23.0%; Pred. No. 1.6e-08;
Matches 60; Conservative 47; Mismatches 90; Indels 64; Gaps 11;

Qy 161 --FISILTF-----KGLISCVNWCYINGRNSDLVLYVTSND--TTVLLPP 206
Db 181 SQPINMMLIFSAFITVLLILKVMFKCVMTCYRFMKHNSA---VEDSSKLFKVALPS 237

Query Match 14.2%; Score 170; DB 11; Length 261;
Best Local Similarity 23.0%; Pred. No. 1.6e-08;
Matches 60; Conservative 47; Mismatches 90; Indels 64; Gaps 11;

Qy 207 YDDA---TVNGAAKEPPPPY 223
Db 238 YEEALSPLTKTPGDPAPPY 258

RESULT 12
Q9BLM6 PRELIMINARY; PRT; 286 AA.
ID Q9BLM6
AC Q9BLM6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)

```

```

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Tripanning orphan receptor.
GN TM3.
OS Schistosoma haematobium (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6185;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92296361; PubMed=10366712;
RA Inal J.M.;
RT "Schistosoma TOR (trispinning orphan receptor), a novel, antigenic
RT surface receptor of the blood-dwelling, Schistosoma parasite.";
RL Biochim. Biophys. Acta 1445:283-298 (1999).
DR EMBL; U57714; AAK11492.1; -
KW Receptor.
SQ SEQUENCE 286 AA; 31755 MW; A188B2046289C248 CRC64;

Query Match 13.1%; Score 157; DB 5; Length 286;
Best Local Similarity 21.6%; Pred. No. 3.1e-07;
Matches 43; Conservative 29; Mismatches 69; Indels 58; Gaps 4;

Qy 74 IATAISLLMILICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYNSIQ 133
Db IATVTTFSLAFCFMVHAAITRQPTHLPPFFIQQVPLIICLIHILGFSSTSDIRLVI 87
Qy 134 RQLPPNPPYRDDVMSNPTCLVLIILFISILITFKGLISCVNVCYRI----- 183
Db 88 HT-----KTGPIYIKSTGTFTIILSICMMLAFKAYCLGWWDCYKYLMLNRGNLLD 140
Qy 184 -----NGRNS-----DVLVVTSTNTVLLPP 206
Db 141 DWYSDQWHLSTFWSLRAGNSGNPNRPNRPTITVDPAND-----LPK 196
Qy 207 YDDATVNGAAKEPPPPYVS 225
Db 197 YEDILKIRNAVAPPYICS 215

RESULT 13
Q8BFZ0 PRELIMINARY; PRT; 261 AA.
AC Q8BFZ0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Lysosomal-associated protein transmembrane 5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK089432; BAC40881.1; -
DR EMBL; AK089535; BAC40917.1; -
SQ SEQUENCE 261 AA; 29619 MW; DC4575620AB40EE5 CRC64;

Query Match 13.0%; Score 156; DB 11; Length 261;
Best Local Similarity 22.4%; Pred. No. 3.5e-07;
Matches 60; Conservative 48; Mismatches 82; Indels 78; Gaps 13;

Qy 14 SCCLCCHVTGTLIGWYLLINAVVLLILSALADPPQYVNFSSSELGGDFEWDANMC 73
Db 11 TCC-CFNIRVATIALIYHMVMS--VLLFIEHV-----EVARGKVCSPFKPFLRMA 61

Query Match 12.2%; Score 146.5; DB 5; Length 281;
Best Local Similarity 20.5%; Pred. No. 3.2e-06;
Matches 41; Conservative 33; Mismatches 67; Indels 59; Gaps 5;

Qy 74 IATAISLLMILICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYNSIQ 133
Db IATVTTFSLAFCFMVHAAITRQPTHLPPFFIQQVPLIICLIHILGFSSTSDIRLMI 87
Qy 134 RQLPPNPPYRDDVMSNPTCLVLIILFISILITFKGLISCVNVCYRI----- 183
Db 88 HT-----KTGPIYIKSTGTFTIILSICMMLAFKAYCLGWWDCYKYLMLNRKNLLD 140
Qy 184 -----NGRNS-----SDVLVVTSTNTVLLPP 206
Db 141 DWYSDQWHLSTFWSLRAGNSGNPNRPNRPTITVDPAND-----LPK 196
Qy 207 YDD-ATVNGAAKEPPPPYVS 225
Db 197 YEDILKIPNAVAPPYICS 216

RESULT 15
Q9VEW3 PRELIMINARY; PRT; 165 AA.
AC Q9VEW3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE CG10311 protein (R861190p).
GN CG10311.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2004, 14:15:55 ; Search time 41 Seconds
(without alignments)
874.932 Million cell updates/sec

Title: US-09-965-529-26
Perfect score: 1200
Sequence: 1 MKMVAPWTRFYSNCLCLCH.....YDDATVNGAKEPPPPYVSA 226

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 19Jun03.*
1: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1200	100.0	226	21 AAY94879	Human protein clon
2	1200	100.0	226	22 ABUS2920	Human intracellula
3	1200	100.0	226	22 AAM39575	Human polypeptide
4	1200	100.0	226	22 AAB74720	Human membrane ass
5	1200	100.0	226	22 AAB88317	Human membrane or
6	1200	100.0	226	23 ABB89618	Human polypeptide
7	1200	100.0	226	24 ABUS6591	Lung cancer-associ
8	1200	100.0	231	22 AAM41361	Human polypeptide
9	1200	100.0	283	23 ABP64704	Human protein SEQ

10	1200	100.0	283	23	ABG96360	Human ovarian can
11	892.5	74.4	301	22	AAU30363	Novel human secret
12	769	64.1	162	23	AAE26970	Human gene 12 enco
13	769	64.1	162	23	AAE27108	Human gene 12 enco
14	769	64.1	162	24	ABU64981	Human secreted pro
15	714	59.5	137	19	AAW75240	Fragment of human
16	714	59.5	137	23	AAE27004	Human gene 12 enco
17	714	59.5	137	23	AAE27142	Human gene 12 enco
18	714	59.5	137	24	ABU65015	Human secreted pro
19	682	56.8	157	20	AAV60445	Human normal bladd
20	553.5	46.1	221	22	ABUS2921	Human intracellula
21	553.5	46.1	233	23	ABB89773	Human polypeptide
22	553.5	46.1	254	21	AAB43823	Human cancer assoc
23	520	43.3	183	20	AAV60444	Human normal bladd
24	515.5	43.0	215	22	AAU12173	Human PRO3574 poly
25	515.5	43.0	215	24	ABU66571	Human PRO polypept
26	515.5	43.0	215	24	ABU66847	Human secreted/tra
27	515.5	43.0	215	24	ABUS9652	Novel secreted and
28	433	36.1	117	23	ABB89228	Human polypeptide
29	417	34.8	87	19	AAW75241	Fragment of human
30	417	34.8	87	23	AAE27005	Human gene 12 enco
31	417	34.8	87	23	AAE27143	Human gene 12 enco
32	417	34.8	87	24	ABU65016	Human secreted pro
33	282.5	23.5	425	22	ABB69779	Drosophila melanog
34	282.5	23.5	432	22	ABB59229	Drosophila melanog
35	230.5	19.2	144	23	ABB89772	Human polypeptide
36	212	17.7	113	23	ABB89067	Human polypeptide
37	195	16.2	56	20	AAV60462	Human normal bladd
38	182.5	15.2	301	21	ABUS8346	Lung cancer associ
39	175.5	14.6	262	19	AAW46577	Human haematopoiet
40	164	13.7	286	22	AAU08262	Schistosoma haemat
41	162.5	13.5	284	22	ABG27227	Novel human diagno
42	157	13.1	286	22	AAU08263	Schistosoma haemat
43	156	13.0	261	19	AAW46578	Mouse haematopoiet
44	146.5	12.2	281	22	AAU08264	Schistosoma manso
45	146.5	12.2	281	22	AAU08271	Schistosoma manso

ALIGNMENTS

RESULT 1

AAAY94879
ID AAY94879 standard; Protein; 226 AA.
AC AAY94879;
XX
XX
XX
DT 12-JUN-2000 (first entry)
DE Human protein clone HP02419.

XX Human protein; hydrophobic domain; nutritional source; haematopoiesis;
cycokine production; cell proliferation; cell differentiation;
immune deficiency; infectious disease; autoimmune disorder; asthma;
multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;
allergic reaction; osteoporosis; osteoarthritis; periodontal disease;
nervous system disorder; Alzheimer's disease; Parkinson's disease;
Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury;
systemic cytokine damage; tissue differentiation; contraceptive injury;
coagulation disorder; myocardial infarction; inflammatory condition;
septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;
nephritis; therapy.

XX Homo sapiens.

OS WO200005367-A2.

PN 03-FEB-2000.

XX 22-JUL-1999; 99WO-JP03929.

XX 24-JUL-1998; 98JP-0208820.

PR 07-AUG-1998; 98JP-0224105.

PR 25-AUG-1998; 98JP-0238116.
PR 09-SEP-1998; 98JP-0254736.
PR 29-SEP-1998; 98JP-0275505.
XX
XX (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
XX
XX Kato S, Kimura T;
XX WPI; 2000-182694/16.
DR
XX Novel human proteins having hydrophobic domains useful for treating
XX osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,
PT multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -
PT
XX Claim 1; Page 275-276; 351pp; English.
XX
XX This sequence represents a human protein of the invention, which has
CC hydrophobic domains. The DNA sequences can be used as a probe or as a
CC genetic marker. The protein can also be used as a marker, and to identify
CC potential genetic disorders. The DNA and protein can also be used as
CC nutritional sources or supplements. The protein exhibits cytokine, cell
CC proliferation, cell differentiation activities and induces production of
CC other cytokines in certain cell populations. The protein also exhibits
CC immune stimulating or immune suppressing activity. It can be used in the
CC treatment of various immune deficiencies and disorders, and to treat
CC infectious diseases caused by viral, bacterial, fungal or other
CC infections. The protein is also used for treating autoimmune disorders,
CC such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid
CC arthritis. It is also useful in the treatment of allergic reactions and
CC conditions such as asthma, and in immune suppression after organ
CC transplantation. The protein is useful in regulation of haematopoiesis
CC and consequently in the treatment of myeloid or lymphoid cell
CC deficiencies. It is also used in compositions for tissue growth or
CC regeneration. The protein is also used in the treatment of osteoporosis
CC or osteoarthritis and in the treatment of periodontal disease and other
CC tooth repair processes. The protein is used in the treatment of nervous
CC system disorders such as Alzheimer's disease, Parkinson's disease, and
CC Huntington's disease. They are useful for protection or regeneration and
CC treatment of lung or liver fibrosis, reperfusion injury in various
CC tissues, and conditions resulting from systemic cytokine damage. They are
CC also used for promoting or inhibiting tissue differentiation. They are
CC also used as contraceptives since they exhibit activin or inhibin related
CC activities and as a fertility inducing therapeutic. They are used for
CC treating various coagulation disorders and in treatment and prevention of
CC conditions resulting from coagulation activities e.g. myocardial
CC infarction or stroke. They also act as receptors, receptor ligands or
CC inhibitors or agonists of receptor/ligand interactions. They are used to
CC treat inflammatory conditions such as septic shock, sepsis, ischaemia
CC reperfusion injury, arthritis, and nephritis. They can be used to
CC prevent tumours.
XX
XX Sequence 226 AA;
Query Match 100.0%; Score 1200; DB 21; Length 226;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKWVAPWTRFYSNCCLCCHVRTGTLIGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Db 1 MKWVAPWTRFYSNCCLCCHVRTGTLIGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60
Qy 61 GGDPEFMDANMCIAISLMLILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDPEFMDANMCIAISLMLILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Qy 121 TVLIYPSNIOEYIRQLPPNPFYRDDVMSVNPCLVLIILFISILITFKGVLISCVWNCY 180
Db 121 TVLIYPSNIOEYIRQLPPNPFYRDDVMSVNPCLVLIILFISILITFKGVLISCVWNCY 180
Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 2

ABUS2920
ID ABUS2920 standard; Protein; 226 AA.

XX AC ABUS2920;
XX
XX
DT 14-APR-2003 (first entry)

XX Human intracellular transport and trafficking protein DKFZphut1_24ell.
XX Human; gene therapy; vaccine; disease treatment; detection.
XX Homo sapiens.

XX WO200112859-A2.

XX 22-FEB-2001.

XX 18-AUG-2000; 2000WO-IB01496.

XX 18-AUG-1999; 99US-0149499.

XX 28-SEP-1999; 99US-0156503.

XX (GSHU-) GERMAN HUMAN GENOME PROJECT.

XX Wiemann S;

XX WPI; 2001-327840/34.

XX N-PSDB; ABX71329.

XX Nucleic acids having the sequences of clones isolated from libraries of
XX different human tissues, useful in recombinant DNA methodologies -

XX Claim 21; Page 534; 1095pp; English.

XX This invention describes novel polynucleotides and polypeptides isolated
XX from human CDNA libraries which can be used for gene therapy or in
XX vaccines. The polynucleotides of the invention and antibodies encoded by
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate polypeptide expression. The products of the
XX invention may also be used to identify modulators of expression and
XX activity and to down regulate expression and activity. The antibodies of
XX the invention may also be used as diagnostic agents for detecting the
XX presence of polypeptides in samples. This sequence represents a
XX polypeptide described in the disclosure of the invention.

XX Sequence 226 AA;

Query Match 100.0%; Score 1200; DB 22; Length 226;

Best Local Similarity 100.0%; Pred. No. 2.4e-125;

Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYSNCCLCCHVRTGTLIGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60

Db 1 MKWVAPWTRFYSNCCLCCHVRTGTLIGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60

Qy 61 GGDPEFMDANMCIAISLMLILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120

Db 61 GGDPEFMDANMCIAISLMLILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120

Qy 121 TVLIYPSNIOEYIRQLPPNPFYRDDVMSVNPCLVLIILFISILITFKGVLISCVWNCY 180

Db 121 TVLIYPSNIOEYIRQLPPNPFYRDDVMSVNPCLVLIILFISILITFKGVLISCVWNCY 180

Qy 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

Db 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226

RESULT 3

AAM39575

AA039575 standard; Protein; 226 AA.
AA039575;
22-OCT-2001 (first entry)
Human polypeptide SEQ ID NO 2720.
Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
peripheral nervous system; neuropathy; central nervous system; CNS;
Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
leukaemia.
Homo sapiens.
WO200153312-A1.
26-JUL-2001.
26-DEC-2000; 2000WO-US34263.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
(HYSE-) HYSEQ INC.
Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
Zhao Q, Zhou P, Goodrich R, Drmanac RT;
WPI; 2001-442253/47.
N-PSDB; AA158731.
Novel nucleic acids and polypeptides, useful for treating disorders
such as central nervous system injuries -
Example 4; SEQ ID NO 2720; 10078pp; English.
The invention relates to human nucleic acids (AA157798-AA161369) and
the encoded polypeptides (AA038642-AA042213) with nootropic,
immunosuppressant and cytostatic activity. The polynucleotides are useful
in gene therapy. A composition containing a polypeptide or polynucleotide
of the invention may be used to treat diseases of the peripheral nervous
system, such as peripheral nervous injuries, peripheral neuropathy and
localised neuropathies and central nervous system diseases, such as
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
utilization of the activities such as: immune system suppression,
Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
and thrombolytic activity, cancer diagnosis and therapy, drug screening,
assays for receptor activity, arthritis and inflammation, leukaemias and
C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
specification.
Sequence 226 AA;
Query Match 100.0%; Score 1200; DB 22; Length 226;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKWAPWTRFYSNCCLCCHVTRTGTLGGVYLIINAVVLLILLSALADPDQYFSSSEL 60
DB 1 MKWAPWTRFYSNCCLCCHVTRTGTLGGVYLIINAVVLLILLSALADPDQYFSSSEL 60

QY 61 GGDFFMDNDANMCIAIAISLLMILI CAMATYGA YKORAAWIIIPFFCYQIFDFALNMLVAI 120
DB 61 GGDFFMDNDANMCIAIAISLLMILI CAMATYGA YKORAAWIIIPFFCYQIFDFALNMLVAI 120
QY 121 TVLIYPNSIOEYIROLPPNPPYRDDVMSVNPTCLVLIILLFISILTFKGYLISCVWNCY 180
DB 121 TVLIYPNSIOEYIROLPPNPPYRDDVMSVNPTCLVLIILLFISILTFKGYLISCVWNCY 180
QY 181 RYINGRNSSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
DB 181 RYINGRNSSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
RESULT 4
AAB74720
ID AAB74720 standard; Protein; 226 AA.
XX AC AAB74720;
XX DT 12-JUN-2001 (first entry)
XX DE Human membrane associated protein MEMAP-26.
XX KW Human; membrane associated protein; MEMAP; diagnosis; cytostatic;
antiinflammatory; anticonvulsant; immunosuppressive; antidiarrhetic;
antiarteriosclerotic; gene therapy; cell proliferative disorder;
KW autoimmune disorder; inflammatory disorder; neurological disorder;
KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;
KW epilepsy; diarrhoea.
XX OS Homo sapiens.
XX PN WO200112662-A2.
XX PD 22-FEB-2001.
XX PF 14-AUG-2000; 2000WO-US22315.
XX PR 17-AUG-1999; 99US-0149641.
XX PR 09-NOV-1999; 99US-0164203.
XX PA (INCY-) INCYTE GENOMICS INC.
XX PI Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;
PI Baughn MR, Lu DAM, Patterson C;
XX WPI; 2001-168860/17.
XX N-PSDB; AAF81766.
Isolated polypeptide with a human membrane associated protein sequence
is useful for the diagnosis, prevention and treatment of cell
proliferative, autoimmune/inflammatory, neurological and
gastrointestinal disorders -
Disclosure; Page 138; 173pp; English.
AAB74720 to AAF81777 encode the human membrane associated proteins
(MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,
antiinflammatory, anticonvulsant, immunosuppressive, antidiarrhetic and
antiarteriosclerotic activities, which can be used in gene therapy.
MEMAPs and agonist of MEMAPs can be used to treat a disease or condition
associated with decreased expression of functional MEMAP and antagonists
of MEMAP are used to treat a disease or condition associated with
overexpression of functional MEMAP. These disorders include cell
proliferative, autoimmune/inflammatory, neurological and gastrointestinal
disorders. The MEMAP polynucleotides and proteins are also used for the
diagnosis of these disorders. Specific examples of these disorders
include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea.
MEMAP proteins can be used to screen for compounds which specifically
bind MEMAP including antibodies, oligonucleotides, proteins and small
molecules. MEMAP polynucleotides can be used to prepare transgenic
animals which can be studied to provide information concerning human
disease. Anti-MEMAP antibodies are useful in immunoassays for the

XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders -
XX
XX
XX Claim 11; SEQ ID NO 1994; 2081pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABL89449-ABL90853) and proteins
CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 226 AA;
Query Match 100.0%; Score 1200; DB 23; Length 226;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKWVAPWTRFYSNCCLCCHVRTGTLIGVWYLIINAVLLILLSALADPDQYVNFSSSEL 60
DB 1 MKWVAPWTRFYSNCCLCCHVRTGTLIGVWYLIINAVLLILLSALADPDQYVNFSSSEL 60
QY 61 GGDPEFDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
DB 61 GGDPEFDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
QY 121 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
DB 121 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
QY 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226
DB 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226
RESULT 7
ABU56591
ID ABU56591 standard; Protein; 226 AA.
XX
XX AC ABU56591;
XX
XX DT 02-APR-2003 (first entry)
XX
XX DE Lung cancer-associated polypeptide #184.
XX
XX Lung cancer-associated polypeptide; cytostatic; emphysema;
KW anti-inflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
XX Unidentified.
OS
XX
XX WO200286443-A2.
PN
XX
XX 31-OCT-2002.
PD
XX
XX 18-APR-2002; 2002WO-US12476.

XX 18-APR-2001; 2001US-284770P.
PR 10-MAY-2001; 2001US-290492P.
PR 09-NOV-2001; 2001US-339245P.
PR 13-NOV-2001; 2001US-350666P.
PR 29-NOV-2001; 2001US-334370P.
PR 12-APR-2002; 2002US-372246P.
XX
XX (EOSB-) BOS BIOTECHNOLOGY INC.
XX
XX Aziz N, Murray R;
XX
XX WPI; 2003-093161/08.
DR N-PSDB; ABX76320.
XX
XX Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer -
XX
XX Claim 27; Page 327; 453pp; English.
XX
XX The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung
CC cancer-associated polynucleotides and polypeptides are used for
CC identifying a compound that modulates a lung cancer-associated
CC polypeptide, for inhibiting proliferation of a lung cancer-associated
CC cell to treat lung cancer in a patient and for treating a mammal having
CC lung cancer by administering a modulatory compound identified. The
CC methods are useful for treating lung cancer, such as small cell lung
CC cancer, non-small cell lung cancer or other benign or precancerous
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences ABU56408-ABU56745 represent lung cancer-associated
CC polypeptides of the invention.
XX
SQ Sequence 226 AA;
Query Match 100.0%; Score 1200; DB 24; Length 226;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKWVAPWTRFYSNCCLCCHVRTGTLIGVWYLIINAVLLILLSALADPDQYVNFSSSEL 60
DB 1 MKWVAPWTRFYSNCCLCCHVRTGTLIGVWYLIINAVLLILLSALADPDQYVNFSSSEL 60
QY 61 GGDPEFDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
DB 61 GGDPEFDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
QY 121 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
DB 121 TVLIYPSNIOEYIRQLPNFPYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWNCY 180
QY 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226
DB 181 RYINGRNSDVLVYVTSNDTTLVLPYDDATVNGAAKEPPPPYVSA 226
RESULT 8
AAM41361
ID AAM41361 standard; Protein; 231 AA.
XX
XX AC AAM41361;
XX
XX DT 22-OCT-2001 (first entry)
XX
XX

DE Human polypeptide SEQ ID NO 6292.

XX Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

XX 09-JUL-2000; 2000US-0598048.

XX 19-JUL-2000; 2000US-0620312.

XX 03-AUG-2000; 2000US-0653450.

XX 14-SEP-2000; 2000US-0682191.

XX 19-OCT-2000; 2000US-0693036.

XX 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

XX N-PSDB; AAI60517.

XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -

XX Example 2; SEQ ID NO 6292; 10078bp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with neurotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed
CC specification.

XX SQ Sequence 231 AA;

Query Match 100.0%; Score 1200; DB 22; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKWAPWTFYNSCCLCHVTRTGILGVWYLIINAVVLLTLLSALADPDQYNFSSEL 60
DB 6 MKWAPWTFYNSCCLCHVTRTGILGVWYLIINAVVLLTLLSALADPDQYNFSSEL 65

QY 61 GGDFFEMDDANNCIAAISLMLILCAMATYGAYKQRAAWIIPFCYQIFDPAIIMLVAI 120
DB 66 GGDFFEMDDANNCIAAISLMLILCAMATYGAYKQRAAWIIPFCYQIFDPAIIMLVAI 125

QY 121 TVLIYVNSIOEYIROLPPNFPYRDDVMVSNPTCLVLIILTFKGLVISCWVNCY 180

Db 126 TVLIYVNSIOEYIROLPPNFPYRDDVMVSNPTCLVLIILTFKGLVISCWVNCY 185

QY 181 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
|||||
186 RYINGRNSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 231
|||||

RESULT 9
ABP64704
ID ABP64704 standard; Protein; 283 AA.

XX ABP64704;

XX 25-FEB-2003 (first entry)

XX Human protein SEQ ID 364.

XX Human; expressed sequence tag; EST;
KW haematopoietic disorder; central nervous system disease; viral infection;
KW peripheral nervous system disease; non-healing wound; infectious disease;
KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;
KW fungal infection; autoimmune disorder; coagulation disorder; neurotropic;
KW antiallergic; antiinflammatory; immunosuppressive; neuroprotective;
KW cytostatic; haemostatic; virucide; antibacterial; fungicide;
KW immunostimulant; cerebroprotective.

XX Homo sapiens.

XX WO200259260-A2.

XX 01-AUG-2002.

XX 16-NOV-2001; 2001WO-US42950.

XX 17-NOV-2000; 2000US-0714936.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;
PI Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;

XX WPI; 2002-590824/63.
N-PSDB; ABQ99290.

XX New isolated polynucleotide, useful in research, diagnostic or
PT therapeutic methods, e.g. preventing or treating disorders involving
PT aberrant protein expression or biological activity -

XX Claim 20; SEQ ID 364; 394pp; English.

XX The present invention relates to novel human coding sequences
CC (ABQ99268-ABQ99608) and proteins (ABP64682-ABP65022). The sequences are
CC useful in therapeutic, diagnostic and research methods. The
CC polynucleotides may be used in the field of molecular biology as
CC hybridisation probes, primers for PCR, for chromosome and gene mapping,
CC for the recombinant production of protein, or in generation of anti-sense
CC DNA or RNA. The polynucleotides are useful in diagnostics as expressed
CC sequence tags (ESTs) for identifying expressed genes or for physical
CC mapping of the human genome. The proteins may be used as molecular weight
CC markers, or as nutritional sources or supplements. The proteins may be
CC used to maintain and expand cell population in a totipotential or
CC pluripotential state useful for re-engineering damaged or diseased
CC tissues, transplantation, manufacture of bio-pharmaceuticals or the
CC development of bio-sensors. The polynucleotides and proteins are useful
CC for preventing, treating or ameliorating disorders involving aberrant
CC protein expression or biological activity, e.g. haematopoietic disorders,
CC central/peripheral nervous system diseases, mechanical and traumatic
CC disorders, non-healing wounds, immune deficiencies and disorders,
CC infectious diseases caused by viral, bacterial or fungal infection,
CC autoimmune disorders, allergic reactions and conditions, coagulation
CC disorders, or cancer. The polynucleotide sequences of the invention were
CC assembled from ESTs isolated mainly by sequencing by hybridisation, and
CC in some cases, sequences obtained from one or more public databases.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 283 AA;
Query Match 100.0%; Score 1200; DB 23; Length 283;
Best Local Similarity 100.0%; Pred. No. 3.1e-125;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKWVAPWTRFYSNCCCHVTRGTTLLGVWYLIINAVLLILLSALADPDQYNSSEL 60
Db 58 MKWVAPWTRFYSNCCCHVTRGTTLLGVWYLIINAVLLILLSALADPDQYNSSEL 117
Qy 61 GGDPEFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 118 GGDPEFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 177
Qy 121 TVLIYPSNIOEYIRQLPPNPPYRDDVMSVNPCTCLVLILFISILTFKGLISCVNWCY 180
Db 178 TVLIYPSNIOEYIRQLPPNPPYRDDVMSVNPCTCLVLILFISILTFKGLISCVNWCY 237
Qy 181 RYINGRNSSDVLVYVTSNDTTLVLLPPYDDATVNGAKEPPPPYVSA 226
Db 238 RYINGRNSSDVLVYVTSNDTTLVLLPPYDDATVNGAKEPPPPYVSA 283

RESULT 10

ABG96360
ID ABG96360 standard; Protein; 283 AA.

XX AC ABG96360;
XX DT 11-DEC-2002 (first entry)
XX DE Human ovarian cancer marker OV53.
XX DE Human; ovarian cancer; marker; cancer; familial history; brain disorder;
KW central nervous system disorder; bacterial meningitis; viral meningitis;
KW Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;
KW brain herniation; inflammation; encephalitis; testicular disorder;
KW nontuberculous granulomatous orchitis; connective tissue disorder;
KW heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;
KW histological type; carcinogenic; ovarian cancer marker.
XX OS Homo sapiens.
XX PN WO200271928-A2.
XX PD 19-SEP-2002.
XX PF 14-MAR-2002; 2002WO-US07826.
XX PR 14-MAR-2001; 2001US-276025P.
XX PR 14-MAR-2001; 2001US-276026P.
XX PR 10-AUG-2001; 2001US-311732P.
XX PR 19-SEP-2001; 2001US-323580P.
XX PR 26-SEP-2001; 2001US-324967P.
XX PR 26-SEP-2001; 2001US-325102P.
XX PR 26-SEP-2001; 2001US-325149P.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;
PI Meyers RE, Morrissey MP, Olandt PJ, Sen A, Vieby PO, Mills GB;
PI Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;
XX DR WPI; 2002-723277/78.
XX DR N-PSDB; ABS76456.
XX PT Assessing whether a patient is afflicted with ovarian cancer, useful in
PT assessing the stage or progression of the disease, comprises comparing
PT the expression level of a cancer marker in a sample from a patient and

PT from a non cancer patient -

XX Disclosure; Page 296-297; 481pp; English.

XX CC The present invention relates to a new method for assessing whether a
XX patient is afflicted with ovarian cancer. The method involves comparing
XX the expression level of a marker in a patient sample and the normal level
XX of expression of the marker in a control non-ovarian cancer sample, where
XX the marker is selected from 363 cancer markers described in the
XX specification. The method of the invention is useful in diagnosing or
XX characterising cancer, in detecting the presence of cancer as early as
XX possible, and the recurrence of ovarian cancer. The method may also be of
XX particular use with patients having an enhanced risk of developing
XX ovarian cancer (e.g. patients having a familial history of ovarian
XX cancer). The cancer markers may be used in the management and treatment
XX of e.g. brain and central nervous system disorders (e.g. bacterial and
XX viral meningitis, Alzheimer's disease or Parkinson's disease), brain
XX disorders (e.g. cerebral oedema, hydrocephalus or brain herniations),
XX inflammations (e.g. bacterial or viral meningitis or encephalitis),
XX testicular disorders (e.g. nontuberculous granulomatous orchitis),
XX connective tissue disorders, or heart disorders (e.g. ischaemic heart
XX disease or atherosclerosis). The compositions and methods may also be
XX used in assessing the histological type of neoplasm associated with
XX ovarian cancer, monitoring the progression of ovarian cancer,
XX determining whether ovarian cancer has metastasized or is likely to
XX metastasize, selecting a composition for inhibiting ovarian cancer,
XX assessing the ovarian carcinogenic potential of a compound, or
XX inhibiting ovarian cancer or at risk of developing ovarian cancer. The
XX present amino acid sequence represents one of the ovarian cancer markers
XX described in the invention.

XX SQ Sequence 283 AA;

Query Match 100.0%; Score 1200; DB 23; Length 283;

Best Local Similarity 100.0%; Pred. No. 3.1e-125;

Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYSNCCCHVTRGTTLLGVWYLIINAVLLILLSALADPDQYNSSEL 60
Db 58 MKWVAPWTRFYSNCCCHVTRGTTLLGVWYLIINAVLLILLSALADPDQYNSSEL 117
Qy 61 GGDPEFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 118 GGDPEFMDANMCIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 177
Qy 121 TVLIYPSNIOEYIRQLPPNPPYRDDVMSVNPCTCLVLILFISILTFKGLISCVNWCY 180
Db 178 TVLIYPSNIOEYIRQLPPNPPYRDDVMSVNPCTCLVLILFISILTFKGLISCVNWCY 237
Qy 181 RYINGRNSSDVLVYVTSNDTTLVLLPPYDDATVNGAKEPPPPYVSA 226
Db 238 RYINGRNSSDVLVYVTSNDTTLVLLPPYDDATVNGAKEPPPPYVSA 283

RESULT 11

AAU30363

ID AAU30363 standard; Protein; 301 AA.

XX AC AAU30363;

XX DT 18-DEC-2001 (first entry)

XX DE Novel human secreted protein #854.

XX KW Human; vaccination; gene therapy; nutritional supplement;

XX KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

XX KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX OS Homo sapiens.

XX PN WO200179449-A2.

XX PD 25-OCT-2001.

XX

XX

OS
YY
HomC

55 YKY

US2002172994-A1.
21-NOV-2002.
11-MAY-2001; 2001US-0852797.
14-MAR-1997; 97US-040710P.
14-MAR-1997; 97US-040762P.
30-MAY-1997; 97US-048100P.
30-MAY-1997; 97US-048189P.
30-MAY-1997; 97US-048357P.
30-MAY-1997; 97US-050934P.
06-JUN-1997; 97US-048970P.
05-SEP-1997; 97US-057765P.
19-DEC-1997; 97US-068368P.
02-FEB-2001; 2001US-265583P.
12-MAR-1998; 98WO-US04858.
11-SEP-1998; 98US-0152060.
(RUBE/) RUBEN S M.
(ROSE/) ROSEN C A.
(LIYU/) LI Y.
(ZENG/) ZENG Z.
(KYAW/) KYAW H.
(FISC/) FISCHER C L.
(LIHH/) LI H.
(SOPP/) SOPPET D R.
(GENT/) GENTZ R L.
(WEIY/) WEI Y.
(MOOR/) MOORE P A.
(YOUN/) YOUNG P E.
(GREE/) GREENE J M.
(FERR/) FERRIE A M.
Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
Ferrie AM;
WPI; 2003-310989/30.
N-PSDB; ABX96977.
New human secreted polypeptides and polynucleotides for diagnosing,
prognosing, preventing and treating immune, hyperproliferative, liver,
kidney, reproductive disorders and for identifying modulators of
therapeutic use -
Claim 11; Page 178; 209pp; English.
The invention relates to an isolated polypeptide comprising an amino acid
sequence at least 95% identical to sequence of 28 human secreted
proteins, their fragment, polypeptide domain, epitope, secreted form,
variant, allelic variant, or species homologue, or the encoded sequence
included in ATCC 9721 and 9722. Also included are the encoding
nucleic acids, recombinant vectors, host cells, antibodies, and genes.
The proteins and nucleic acids are useful for diagnosing, preventing,
treating, prognosing or ameliorating a medical condition e.g.
immunodeficiencies (e.g. X-linked agammaglobulinaemia, B cell
immunodeficiencies, severe combined immunodeficiencies), autoimmune
disorders (e.g. systemic erythematous, rheumatoid arthritis, multiple
sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia,
Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis),
haematopoietic disorders, inflammatory conditions (e.g. septic shock,
sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease),
respiratory disorders (e.g. asthma and allergy), gastrointestinal
disorders, cancers (e.g. gastric, ovarian, lung, bladder, liver and
breast), central nervous system (CNS) disorders (e.g. ischaemic brain
injury and/or stroke, traumatic brain injury), neurodegenerative
disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related
dementia, and prion disease), cardiovascular disorders (e.g.
atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary
bypass complications), inflammation (e.g. hepatitis, gout, trauma,
pancreatitis, sarcoidosis, dermatitis, allogeneic transplant rejection),
blood-related disorders (thrombosis, arterial thrombosis),
hyperproliferative disorders, renal disorders (e.g. acute
glomerulonephritis), endocrine disorders (e.g. Addison's disease,
hyperthyroidism, hyperpituitarism), liver diseases and disorders,
reproductive system disorders (e.g. endometriosis), infectious diseases,
and pancreatic disorders. Many other diseases and disorders are listed in
the specification. They also useful as a vaccine adjuvant. Further they
are useful to enhance or inhibit complement mediated cell lysis, for
stimulating wound and tissue repair, angiogenesis, and the repair of
vascular or lymphatic diseases or disorders. They are also useful
to prevent hair loss, to modulate mammalian characteristics such as body
height, weight, hair colour, and to increase or decrease storage
capabilities, fat content, lipid, protein, carbohydrate, vitamins,
minerals, cofactors or other nutritional components. The proteins are
also useful for identifying binding partners. The present sequence
represents a secreted protein of the invention.
SQ Sequence 162 AA;
Query Match 64.1%; Score 769; DB 24; Length 162;
Best Local Similarity 99.3%; Pred. No. 1.7e-77;
Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKWVAPWTRFYSNSCCLCCHVTRGTLLGVWYLIINAVLLILLSALADPDQYNSSEL 60
DB 1 MKWVAPWTRFYSNSCCLCCHVTRGTLLGVWYLIINAVLLILLSALADPDQYNSSEL 60
QY 61 GGDPEFMDANMCIAIAISLLMILICAMATYGAAYKQRAAWIIPFFCYQIFDFALNMLVAI 120
DB 61 GGDPEFMDANMCIAIAISLLMILICAMATYGAAYKQRAAGIIPFFCYQIFDFALNMLVAI 120
QY 121 TVLIYPSNIOEYIRQLPPNPPYRDDVM 147
DB 121 TVLIYPSNIOEYIRQLPPNPPYRDDVM 147
RESULT 15
AAW75240
ID AAW75240 standard; Protein; 137 AA.
XX AC AAW75240;
XX DT 29-JAN-1999 (first entry)
XX DE DE
XX KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
XX KW developmental abnormality; foetal deficiency; blood; allergy; renal;
XX KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
XX KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
XX KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX OS Homo sapiens.
XX PN WO9840483-A2.
XX PD 17-SEP-1998.
XX PF 12-MAR-1998; 98WO-US04858.
XX PR 19-DEC-1997; 97US-0068368.
XX PR 14-MAR-1997; 97US-0040710.
XX PR 14-MAR-1997; 97US-0040762.
XX PR 30-MAY-1997; 97US-0048100.
XX PR 30-MAY-1997; 97US-0048189.
XX PR 30-MAY-1997; 97US-0048357.
XX PR 06-JUN-1997; 97US-0050934.
XX PR 05-SEP-1997; 97US-0048970.
XX (HUMA-) HUMAN GENOME SCI INC.
PA

XX Ferrie AM, Fischer CL, Gentz RL, Greene JM, Kyaw H;
PI Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR;
PI Wei YP, Young PE, Zeng Z;
XX WPI; 1998-520811/44.
DR N-PSDB; AAV34297.
XX
XX Isolated human polynucleotide(s) encoding secretory peptide(s) -
PT used to develop products for the diagnosis and treatment of e.g.
PT inflammation, cancers, CNS disorders or immune system disorders
XX
XX Disclosure; Page 14; 20pp; English.
XX
XX This sequence represents a fragment of a secreted human protein encoded
CC by the nucleic acid molecule designated Gene 12 (AAV34297). The gene
CC can be used to generate fusion proteins by linking to the gene to a
CC human immunoglobulin Fc portion (e.g. AAV34277) for increasing the
CC stability of the fused protein as compared to the human protein only.
CC The invention relates to 28 novel genes and their fragments (nucleic
CC acid sequences: AAV34286-V34325; amino acid sequences AAW75196-W75235)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 28
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV34286 for described uses).
XX
SQ Sequence 137 AA;
Query Match 59.5%; Score 714; DB 19; Length 137;
Best Local Similarity 99.3%; Pred. No. 1.9e-71;
Matches 136; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 RFYSNSCLCCHVRTGTTLLGWYLLINAVVLLILLSALADPDQYNFSSSELGGDFEFD 68
Db 1 RFYSNSCLCCHVRTGTTLLGWYLLINAVVLLILLSALADPDQYNFSSSELGGDFEFD 60
Qy 69 DANMCIAIAISLLMILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAITVLIYPS 128
Db 61 DANMCIAIAISLLMILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAITVLIYPS 120
Qy 129 IQEYIRQLPPNPPYRDD 145
Db 121 IQEYIRQLPPNPPYRDD 137

Search completed: February 2, 2004, 14:21:52
Job time : 43 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2004, 14:23:16 ; Search time 33 Seconds
(without alignments)
1423.280 Million cell updates/sec

Title: US-09-965-529-26
Perfect score: 1200
Sequence: 1 MKWAPWTRFYSNCLCCH.....YDDATVNGAAKEPPPYVSA 226

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 789580 seqs, 207824079 residues

Total number of hits satisfying chosen parameters: 789580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1200	100.0	226	10	US-09-965-529-26 Sequence 26, Appl
2	1200	100.0	226	11	US-09-969-680A-26 Sequence 26, Appl
3	1200	100.0	226	12	US-10-264-237-1994 Sequence 1994, Ap
4	1200	100.0	283	12	US-10-301-822-99 Sequence 99, Appl
5	1200	100.0	283	15	US-10-097-340-175 Sequence 175, App
6	769	64.1	162	9	US-09-853-161-63 Sequence 63, Appl
7	769	64.1	162	9	US-09-852-659A-63 Sequence 63, Appl
8	769	64.1	162	10	US-09-852-797-63 Sequence 63, Appl
9	714	59.5	137	9	US-09-853-161-97 Sequence 97, Appl
10	714	59.5	137	9	US-09-852-659A-97 Sequence 97, Appl
11	714	59.5	137	10	US-09-852-797-97 Sequence 12, Appl
12	553.5	46.1	233	12	US-10-376-564-12 Sequence 12, Appl
13	553.5	46.1	233	12	US-10-264-237-2149 Sequence 2149, Ap
14	553.5	46.1	254	9	US-09-925-301-1268 Sequence 1268, Ap
15	541.5	45.1	233	12	US-10-376-564-11 Sequence 11, Appl

16	515.5	43.0	215	12	US-10-137-870-4	Sequence 4, Appli
17	515.5	43.0	215	12	US-10-140-018-4	Sequence 4, Appli
18	515.5	43.0	215	12	US-10-140-021-4	Sequence 4, Appli
19	515.5	43.0	215	12	US-10-140-274-4	Sequence 4, Appli
20	515.5	43.0	215	12	US-10-140-471-4	Sequence 4, Appli
21	515.5	43.0	215	12	US-10-140-807-4	Sequence 4, Appli
22	515.5	43.0	215	12	US-10-140-922-4	Sequence 4, Appli
23	515.5	43.0	215	12	US-10-140-924-4	Sequence 4, Appli
24	515.5	43.0	215	12	US-10-140-926-4	Sequence 4, Appli
25	515.5	43.0	215	12	US-10-141-698-4	Sequence 4, Appli
26	515.5	43.0	215	12	US-10-141-702-4	Sequence 4, Appli
27	515.5	43.0	215	12	US-10-141-704-4	Sequence 4, Appli
28	515.5	43.0	215	12	US-10-142-421-4	Sequence 4, Appli
29	515.5	43.0	215	12	US-10-142-432-4	Sequence 4, Appli
30	515.5	43.0	215	12	US-10-142-767-4	Sequence 4, Appli
31	515.5	43.0	215	12	US-10-143-033-4	Sequence 4, Appli
32	515.5	43.0	215	12	US-10-144-994-4	Sequence 4, Appli
33	515.5	43.0	215	12	US-10-145-628-4	Sequence 4, Appli
34	515.5	43.0	215	12	US-10-145-631-4	Sequence 4, Appli
35	515.5	43.0	215	12	US-10-145-633-4	Sequence 4, Appli
36	515.5	43.0	215	12	US-10-145-746-4	Sequence 4, Appli
37	515.5	43.0	215	12	US-10-145-748-4	Sequence 4, Appli
38	515.5	43.0	215	12	US-10-145-823-4	Sequence 4, Appli
39	515.5	43.0	215	12	US-10-145-828-4	Sequence 4, Appli
40	515.5	43.0	215	12	US-10-145-870-4	Sequence 4, Appli
41	515.5	43.0	215	12	US-10-145-876-4	Sequence 4, Appli
42	515.5	43.0	215	12	US-10-145-959-4	Sequence 4, Appli
43	515.5	43.0	215	12	US-10-146-724-4	Sequence 4, Appli
44	515.5	43.0	215	12	US-10-146-725-4	Sequence 4, Appli
45	515.5	43.0	215	12	US-10-146-795-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-965-529-26
; Sequence 26, Application US/09965529
; Publication No. US20020182671A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Yaida
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dyoung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PP-0731 USA
; CURRENT APPLICATION NUMBER: US/09/965,529
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 26
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 2795577CD1
US-09-965-529-26

Query Match 100.0%; Score 1200; DB 10; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.5e-115;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKWAPWTRFYSNCLCCHVTRGTILLGVYLIINAVVILLISALADPPQYNFSSSEL 60

Db 1 MKWAPWTRFYSNCLCCHVTRGTILLGVYLIINAVVILLISALADPPQYNFSSSEL 60

Qy 1 MKWVAPWTRFYSNSCCLCHVRTGTTILGVWYLIINAVVLLILSALADPDQYNFSSSEL 60
Db 58 MKWVAPWTRFYSNSCCLCHVRTGTTILGVWYLIINAVVLLILSALADPDQYNFSSSEL 117
Qy 61 GGDFEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 118 GGDFEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 177
Qy 121 TVLIYFNSIOEYIRQLPFPNPFYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWCY 180
Db 178 TVLIYFNSIOEYIRQLPFPNPFYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWCY 237
Qy 181 RYINGRNSSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

RESULT 5

US-10-097-340-175
; Sequence 175, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-175

Query Match 100.0%; Score 1200; DB 15; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKWVAPWTRFYSNSCCLCHVRTGTTILGVWYLIINAVVLLILSALADPDQYNFSSSEL 60
Db 58 MKWVAPWTRFYSNSCCLCHVRTGTTILGVWYLIINAVVLLILSALADPDQYNFSSSEL 117

Qy 61 GGDFEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 118 GGDFEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 177
Qy 121 TVLIYFNSIOEYIRQLPFPNPFYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWCY 180
Db 178 TVLIYFNSIOEYIRQLPFPNPFYRDDVMSVNPCTCLVLIILFISILTFKGYLISCVWCY 237
Qy 181 RYINGRNSSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 238 RYINGRNSSDVLVYVTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 283

RESULT 6

US-09-853-161-63
; Sequence 63, Application US/09853161
; Patent No. US20020076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-63

Query Match 64.1%; Score 769; DB 9; Length 162;
Best Local Similarity 99.3%; Pred. No. 2.6e-71;
Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKWVAPWTRFYSNSCCLCHVRTGTTILGVWYLIINAVVLLILSALADPDQYNFSSSEL 60
Db 1 MKWVAPWTRFYSNSCCLCHVRTGTTILGVWYLIINAVVLLILSALADPDQYNFSSSEL 60
Qy 61 GGDFEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Db 61 GGDFEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
Qy 121 TVLIYFNSIOEYIRQLPFPNPFYRDDVM 147
Db 121 TVLIYFNSIOEYIRQLPFPNPFYRDDVM 147

RESULT 7

US-09-852-659A-63

Sequence 63, Application US/09852659A
Patent No. US20020077287A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P4
CURRENT APPLICATION NUMBER: US/09/852,659A
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: PCT/US98/04858
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,710
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/050,934
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: PCT/US98/04858
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,357
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/057,765
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/068,368
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 63
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-09-852-659A-63

Query Match 64.1%; Score 769; DB 9; Length 162;
Best Local Similarity 99.3%; Pred. No. 2.6e-71;
Matches 146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKWVAPWTRFYNSCCLCCHVRTGILLGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60
DB 1 MKWVAPWTRFYNSCCLCCHVRTGILLGVWYLIINAVVLLILLSALADPDQYNFSSSEL 60

QY 61 GGDFFEMDDANNCTAIAISLLMILICAMATYGAYKQRAAWIIPFCYQIFDFALNMLVAI 120
DB 61 GGDFFEMDDANNCTAIAISLLMILICAMATYGAYKQRAAGIIPFCYQIFDFALNMLVAI 120

QY 121 TVLIYPSNIOEYIROLPPNFPYRDDVM 147
DB 121 TVLIYPSNIOEYIROLPPNFPYRDDVM 147

RESULT 8
US-09-852-797-63
Sequence 63, Application US/09852797
Patent No. US20020172994A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P2
CURRENT APPLICATION NUMBER: US/09/852,797
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: PCT/US98/04858

US-09-852-659A-63

Sequence 63, Application US/09852659A
Patent No. US20020077287A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P3
CURRENT APPLICATION NUMBER: US/09/853,161
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: PCT/US98/04858
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,710
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/050,934
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,357
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/057,765

US-09-852-797-63

Sequence 63, Application US/09852797
Patent No. US20020172994A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P3
CURRENT APPLICATION NUMBER: US/09/853,161
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: PCT/US98/04858
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,710
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/050,934
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,357
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/057,765

```
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 97
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-97

Query Match      59.5%; Score 714; DB 9; Length 137;
Best Local Similarity 99.3%; Pred. No. 9.7e-66;
Matches 136; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 RFYNSCCLCCHVRTGTTLLGWYLIINAVVLLILLSALADPDQYNFSSSELGGDFEFD 68
Db 1 RFYNSCCLCCHVRTGTTLLGWYLIINAVVLLILLSALADPDQYNFSSSELGGDFEFD 60

Qy 69 DANMCIAIAISLLMILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAITVLIYNS 128
Db 61 DANMCIAIAISLLMILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAITVLIYNS 120

Qy 129 IQEYIROLPPNFPYRDD 145
Db 121 IQEYIROLPPNFPYRDD 137

RESULT 10
US-09-852-659A-97
; Sequence 97, Application US/09853659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 97
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-97

Query Match      59.5%; Score 714; DB 9; Length 137;
Best Local Similarity 99.3%; Pred. No. 9.7e-66;
Matches 136; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 RFYNSCCLCCHVRTGTTLLGWYLIINAVVLLILLSALADPDQYNFSSSELGGDFEFD 68
Db 1 RFYNSCCLCCHVRTGTTLLGWYLIINAVVLLILLSALADPDQYNFSSSELGGDFEFD 60

Qy 69 DANMCIAIAISLLMILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAITVLIYNS 128
Db 61 DANMCIAIAISLLMILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAITVLIYNS 120

Qy 129 IQEYIROLPPNFPYRDD 145
Db 121 IQEYIROLPPNFPYRDD 137

RESULT 11
US-09-852-797-97
; Sequence 97, Application US/09852797
; Patent No. US20020172994A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 97
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-797-97

Query Match      59.5%; Score 714; DB 10; Length 137;
Best Local Similarity 99.3%; Pred. No. 9.7e-66;
Matches 136; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 RFYNSCCLCCHVRTGTTLLGWYLIINAVVLLILLSALADPDQYNFSSSELGGDFEFD 68
Db 1 RFYNSCCLCCHVRTGTTLLGWYLIINAVVLLILLSALADPDQYNFSSSELGGDFEFD 60

Qy 69 DANMCIAIAISLLMILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAITVLIYNS 128
Db 61 DANMCIAIAISLLMILICAMATYGAYKORAAWIIPFCYQIFDFALNMLVAITVLIYNS 120

Qy 129 IQEYIROLPPNFPYRDD 145
Db 121 IQEYIROLPPNFPYRDD 137
```

```
RESULT 12
US-10-376-564-12
; Sequence 12, Application US/10376564
; Publication No. US20030180302A1
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckhard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jörn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; the Diagnosis or Treatment of Skin Disorders and Wound
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
; TITLE OF INVENTION: Active Substances
; FILE REFERENCE: 50125/014003
; CURRENT APPLICATION NUMBER: US/10/376,564
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 09/886,319
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 100 30 149.5-41
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-376-564-12

Query Match          46.1%; Score 553.5; DB 12; Length 233;
Best Local Similarity 45.2%; Pred. No. 6.3e-49;
Matches 104; Conservative 45; Mismatches 60; Indels 21; Gaps 6;

QY      9 RFYSNSCLCCHVRTGTLIGVWYLIINAVVLLILLSALADPD-----QY-----NFSS 57
Db      13 RFYSTRCCGCHVRTGTIIIGTWVNVNLLMAILLTVETHPNMSPAVNIQYEVIGNYS 72

QY      58 SELGGDFEFMDANMCIAISLMLICAMATYGAQKRAAWIIPFCYQIFDFALNML 117
Db      73 SERMAD-----NACVLFAVSVLMFTISSMLVGYAISYQVGMILPFCYRLDFVLSCL 125

QY      118 VAITVLIYPNSIOEYIRQLPNFPYRDDVMSVNPCTCLVLIILLFISILTFKGYLISCVW 177
Db      126 VAISSTLYLPRIKEYLDQL-PDPFYKDDLLALDSSCLLFVLVFFALFIIFKAYLINCVW 184

QY      178 NCYRYINGRNSSDVLVY-VTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db      185 NCYKYNRRNVPEIAVPAFAEPQYVLPYEMA-VKMPEKEPPPPYLP 233

RESULT 13
US-10-264-237-2149
; Sequence 2149, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2149
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-2149

Query Match          46.1%; Score 553.5; DB 9; Length 254;
Best Local Similarity 45.2%; Pred. No. 6.9e-49;
Matches 104; Conservative 45; Mismatches 60; Indels 21; Gaps 6;

QY      9 RFYSNSCLCCHVRTGTLIGVWYLIINAVVLLILLSALADPD-----QY-----NFSS 57
Db      34 RFYSTRCCGCHVRTGTIIIGTWVNVNLLMAILLTVETHPNMSPAVNIQYEVIGNYS 93

QY      58 SELGGDFEFMDANMCIAISLMLICAMATYGAQKRAAWIIPFCYQIFDFALNML 117
Db      94 SERMAD-----NACVLFAVSVLMFTISSMLVGYAISYQVGMILPFCYRLDFVLSCL 146

QY      118 VAITVLIYPNSIOEYIRQLPNFPYRDDVMSVNPCTCLVLIILLFISILTFKGYLISCVW 177
Db      147 VAISSTLYLPRIKEYLDQL-PDPFYKDDLLALDSSCLLFVLVFFALFIIFKAYLINCVW 205

QY      178 NCYRYINGRNSSDVLVY-VTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db      206 NCYKYNRRNVPEIAVPAFAEPQYVLPYEMA-VKMPEKEPPPPYLP 254

RESULT 14
US-09-925-301-1268
; Sequence 1268, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1268
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1268

Query Match          46.1%; Score 553.5; DB 9; Length 254;
Best Local Similarity 45.2%; Pred. No. 6.9e-49;
Matches 104; Conservative 45; Mismatches 60; Indels 21; Gaps 6;

QY      9 RFYSNSCLCCHVRTGTLIGVWYLIINAVVLLILLSALADPD-----QY-----NFSS 57
Db      34 RFYSTRCCGCHVRTGTIIIGTWVNVNLLMAILLTVETHPNMSPAVNIQYEVIGNYS 93

QY      58 SELGGDFEFMDANMCIAISLMLICAMATYGAQKRAAWIIPFCYQIFDFALNML 117
Db      94 SERMAD-----NACVLFAVSVLMFTISSMLVGYAISYQVGMILPFCYRLDFVLSCL 146

QY      118 VAITVLIYPNSIOEYIRQLPNFPYRDDVMSVNPCTCLVLIILLFISILTFKGYLISCVW 177
Db      147 VAISSTLYLPRIKEYLDQL-PDPFYKDDLLALDSSCLLFVLVFFALFIIFKAYLINCVW 205

QY      178 NCYRYINGRNSSDVLVY-VTSNDTTLVLLPPYDDATVNGAAKEPPPPYVSA 226
Db      206 NCYKYNRRNVPEIAVPAFAEPQYVLPYEMA-VKMPEKEPPPPYLP 254

RESULT 15
US-10-376-564-11
; Sequence 11, Application US/10376564
; Publication No. US20030180302A1
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckhard
```

; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jorn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
; TITLE OF INVENTION: Active Substances
; FILE REFERENCE: 50125/014003
; CURRENT APPLICATION NUMBER: US/10/376,564
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 09/886,319
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 100 30 149.5-41
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-376-564-11

Query Match 45.1%; Score 541.5; DB 12; Length 233;
Best Local Similarity 44.8%; Pred. No. 1.1e-47;
Matches 103; Conservative 44; Mismatches 62; Indels 21; Gaps 6;
Qy 9 RFSNSCCLCHVGTGILLGWYLIINAVVLLILLSALADPD-----QY----NFSS 57
Db 13 RPYSTRCCGCPHRTGIIILGTWYVWVNLMAILTVEVTHPSMPAVNIQYEVIGNYS 72
Qy 58 SELGDFEEMDDANNCIAIAISLLMILICATYCAKQRAAWIIPFCYQIFDPALNML 117
Db 73 SERMAD-----NACVLFAVSVLMFISSMLVYGAISYQVGLIIPFCYELDFVLSC 125
Qy 118 VAITVLIYPNSIQEYIROLPNFPVRDDVMSVNPCTCLVLIILLFISILTEKYLISCW 177
Db 126 VAISLTYLPRIKEYLDQL-PDPYKDDLALDSSCLLFVLVFFVVFVFIIFKAYLINCW 184
Qy 178 NCYRYINGRNSSDVLVY-VTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA 226
Db 185 NCYKYINNRNVPEIAVYPAETPPQYVLPPTYEMA-VKIPEKEPPPPYVSA 233

Search completed: February 2, 2004, 14:28:48
Job time : 34 secs

THIS PAGE BLANK (USPTO)